

SCORE Search Results Details for Application 10088319 and Search Result us-10-088-319- 2_copy_331_455.rge.

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This page gives you Search Results detail for the Application 10088319 and Search Result us-10-088-319-2_copy_331_455.rge.

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 25, 2006, 09:55:26 ; Search time 1771 Seconds
(without alignments)
4012.101 Million cell updates/sec

Title: US-10-088-319-2_COPY_331_455
Perfect score: 125
Sequence: 1 caaaaacaaaaaacctttac.....tgagtaaggtggccactttg 125

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	124	99.2	652	8	D50607	D50607 Human CD40
	2	124	99.2	1313	8	HUMCD40L5P	L47983 Homo sapien
	3	124	99.2	151978	14	CT005235	CT005235 Pan trogl
	4	124	99.2	175706	8	AL135783	AL135783 Human DNA
c	5	115	92.0	259175	14	AC106521	AC106521 Rattus no
	6	113.4	90.7	205673	14	AC124137	AC124137 Rattus no
	7	112	89.6	2395	6	AR350233	AR350233 Sequence
	8	112	89.6	2395	6	AR629955	AR629955 Sequence
	9	112	89.6	2395	6	AX351057	AX351057 Sequence
	10	112	89.6	6653	8	D31797	D31797 Homo sapien
	11	109.8	87.8	1878	4	AY333790	AY333790 Canis fam
	12	109.8	87.8	1878	6	BD211546	BD211546 Canine an
c	13	109.8	87.8	1878	6	BD211547	BD211547 Canine an
	14	109.8	87.8	1878	6	AR241524	AR241524 Sequence
c	15	109.8	87.8	1878	6	AR241525	AR241525 Sequence
	16	109.8	87.8	1878	6	AR254480	AR254480 Sequence
c	17	109.8	87.8	1878	6	AR254481	AR254481 Sequence
	18	100.8	80.6	213937	9	AL672128	AL672128 Mouse DNA
	19	97.8	78.2	2011	9	S71858S1	S71858 Mus musculu
	20	97	77.6	620	6	E09510	E09510 DNA encodin
	21	93.6	74.9	7057	6	AX251355	AX251355 Sequence
	22	93.6	74.9	7057	6	AX252056	AX252056 Sequence
	23	93.6	74.9	7057	6	AX281483	AX281483 Sequence
	24	93.6	74.9	7057	6	AX346750	AX346750 Sequence
	25	93.6	74.9	7057	6	AX348839	AX348839 Sequence
c	26	84.6	67.7	7057	6	AX251356	AX251356 Sequence
c	27	84.6	67.7	7057	6	AX252057	AX252057 Sequence
c	28	84.6	67.7	7057	6	AX281484	AX281484 Sequence
c	29	84.6	67.7	7057	6	AX346751	AX346751 Sequence
c	30	84.6	67.7	7057	6	AX348840	AX348840 Sequence
	31	37	29.6	37	6	AR629961	AR629961 Sequence
	32	37	29.6	37	6	AX351063	AX351063 Sequence
	33	34.2	27.4	200393	9	AC161601	AC161601 Mus muscu
c	34	34.2	27.4	206959	9	AC157917	AC157917 Mus muscu
c	35	33.6	26.9	226256	9	AC073599	AC073599 Mus muscu
c	36	33.6	26.9	233165	14	AC162370	AC162370 Mus muscu
	37	32.8	26.2	11435	1	U32753	U32753 Haemophilus
	38	32.8	26.2	110000	6	BD426631_07	Continuation (8 of
	39	32.8	26.2	110000	6	AR274513_07	Continuation (8 of
	40	32.8	26.2	110000	6	AR632719_07	Continuation (8 of
	41	32.2	25.8	184287	14	AC154708	AC154708 Mus muscu
	42	32.2	25.8	309506	9	AY363102S1	AY363102 Mus muscu
c	43	32	25.6	195169	9	AC108836	AC108836 Mus muscu
	44	31.6	25.3	242949	14	AC116255	AC116255 Rattus no
c	45	31.4	25.1	124964	8	AL159154	AL159154 Human DNA

ALIGNMENTS

RESULT 1
D50607

LOCUS D50607 652 bp DNA linear PRI 10-FEB-1999
 DEFINITION Human CD40 ligand (hCD40L) gene, 5'-flanking region.
 ACCESSION D50607
 VERSION D50607.1 GI:849048
 KEYWORDS CD40 ligand; hCD40L; type-II membrane glycoprotein.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCE 1 (bases 1 to 652)
 AUTHORS Seyama,K., Kira,S., Ishidoh,K., Souma,S., Miyakawa,T. and
 Kominami,E.
 TITLE Genomic structure and PCR-SSCP analysis of the human CD40 ligand
 gene: its application to prenatal screening for X-linked hyper-IgM
 syndrome
 JOURNAL Hum. Genet. 97 (2), 180-185 (1996)
 PUBMED 8566950
 REFERENCE 2 (bases 1 to 652)
 AUTHORS Ishidoh,K.
 TITLE Direct Submission
 JOURNAL Submitted (19-MAY-1995) Kazumi Ishidoh, Juntendo University School
 of Medicine, Department of Biochemistry; 2-1-1 Hongo, Bunkyo-ku,
 Tokyo 113, Japan (Tel:03-5802-1031, Fax:03-5802-5889)
 FEATURES Location/Qualifiers
 source 1..652
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /cell_type="lymphocyte and placenta"
 protein_bind 270..285
 /bound_moiety="NF-AT"
 protein_bind 315..329
 /bound_moiety="NF-AT"
 protein_bind 511..516
 /bound_moiety="NF-AT"
 TATA_signal 555..563
 misc_feature 585
 /note="transcription start site"
 /evidence=experimental
 misc_feature 588
 /note="transcription start site"
 /evidence=experimental
 misc_feature 652
 /note="translation start site"

ORIGIN

Query Match 99.2%; Score 124; DB 8; Length 652;
 Best Local Similarity 100.0%; Pred. No. 1.7e-29;
 Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AAAAACAAAAACCTTTACGTAACGTTTTTGGCTGGGAGAGAAGACTACGAAGCACATTTT 61
 |||
 Db 462 AAAAACAAAAACCTTTACGTAACGTTTTTGGCTGGGAGAGAAGACTACGAAGCACATTTT 521
 Qy 62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAATAATCCTGAGTAAGGTGGCCAC 121
 |||
 Db 522 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAATAATCCTGAGTAAGGTGGCCAC 581
 Qy 122 TTTG 125
 |||

Db 582 TTTG 585

RESULT 2

HUMCD40L5P

LOCUS HUMCD40L5P 1313 bp DNA linear PRI 06-FEB-2001

DEFINITION Homo sapiens CD40 ligand gene, promoter and partial cds.

ACCESSION L47983

VERSION L47983.1 GI:1129041

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 1313)

AUTHORS Schubert, L.A., King, G., Cron, R.Q., Lewis, D.B., Aruffo, A. and
Hollenbaugh, D.

TITLE The human gp39 promoter. Two distinct nuclear factors of activated
T cell protein-binding elements contribute independently to
transcriptional activation

JOURNAL J. Biol. Chem. 270 (50), 29624-29627 (1995)

PUBMED 8530342

REFERENCE 2 (bases 1 to 1313)

AUTHORS Schubert, L.A., King, G., Cron, R.Q., Lewis, D.B., Aruffo, A. and
Hollenbaugh, D.

TITLE Direct Submission

JOURNAL Submitted (20-DEC-1995) Dept of Pediatrics, Stanford University,
300 Pasteur Drive CCSR Bldg Room 2115b, Stanford, CA 94305, USA

FEATURES Location/Qualifiers

source 1..1313
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
promoter <1..1227
mRNA 1228..>1313
/product="CD40 ligand"
5'UTR 1228..1294
CDS 1295..>1313
/codon_start=1
/product="CD40 ligand"
/protein_id="AAC41932.1"
/db_xref="GI:1129042"
/translation="MIETYN"

ORIGIN

Query Match 99.2%; Score 124; DB 8; Length 1313;
Best Local Similarity 100.0%; Pred. No. 1.7e-29;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      2  AAAAACAAAAACCTTTACGTAACGTTTTTGTCTGGGAGAGAAGACTACGAAGCACATTTT 61
      |||
Db      1105 AAAAACAAAAACCTTTACGTAACGTTTTTGTCTGGGAGAGAAGACTACGAAGCACATTTT 1164

Qy      62  CCAGGAAGTGTTGGGCTGCAACGATTGTGCGCTCTTAATAATCCTGAGTAAGGTGGCCAC 121
      |||
Db      1165 CCAGGAAGTGTTGGGCTGCAACGATTGTGCGCTCTTAATAATCCTGAGTAAGGTGGCCAC 1224

Qy      122  TTTG 125
      |||
Db      1225 TTTG 1228
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RESULT 3
 CT005235
 LOCUS CT005235 151978 bp DNA linear HTG 14-JUN-2005
 DEFINITION Pan troglodytes chromosome X clone RP43-015P08 map Xq28, ***
 SEQUENCING IN PROGRESS ***, 5 unordered pieces.
 ACCESSION CT005235
 VERSION CT005235.1 GI:67772562
 KEYWORDS HTG; HTGS_PHASE1.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Pan.
 REFERENCE 1 (bases 1 to 151978)
 AUTHORS Scheer, S., Kuhl, H., Kube, M., Mueller, I., Thiel, J., Borzym, K.,
 Klages, S., Sontag, M., Kosiura, A., Sudbrak, R., Beck, A., Lehrach, H.,
 Yaspo, M.L. and Reinhardt, R.
 TITLE Direct Submission
 JOURNAL Submitted (14-JUN-2005)
 COMMENT ----- Genome Center
 Center: Max-Planck-Institute for Molecular Genetics
 Center code: MPIMG
 ----- Project Information
 Center clone name: RP43-015P08
 ----- Summary Statistics
 Sequencing vector: pUC19; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 149183 bases at least Q40
 Consensus quality: 149379 bases at least Q30
 Consensus quality: 149536 bases at least Q20
 Quality coverage: 6.9

 This sequence was finished as follows unless otherwise noted: all
 regions were double stranded, sequenced with an alternate
 chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

 The RPCI-43 chimpanzee BAC library was prepared from DNA isolated from the blood of a single male chimpanzee using published protocols (Osoegawa, K. et al. Genomics 51:1-8). The DNA from the chimpanzee ('Clint') was obtained from the Yerkes Primate Center in Atlanta. The library was prepared by Baoli Zhu, Chung Li Shu, Kazutoyo Osoegawa, Evan Eichler & Pieter J de Jong. The library characteristics are described at <http://www.chori.org/bacpac/mchimp43.htm>. The clone may be obtained from Pieter J. de Jong and coworkers (<http://www.chori.org/bacpac>).
 VECTOR: pBACe3.
 contig 01 1. .14831
 contig 02 14932. .33675
 contig 03 33776. .60588
 contig 04 60689. .99409
 contig 05 99510. .151978.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 5 contigs. The true order of the pieces

* is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 14831: contig of 14831 bp in length
 * 14832 14931: gap of unknown length
 * 14932 33675: contig of 18744 bp in length
 * 33676 33775: gap of unknown length
 * 33776 60588: contig of 26813 bp in length
 * 60589 60688: gap of unknown length
 * 60689 99409: contig of 38721 bp in length
 * 99410 99509: gap of unknown length
 * 99510 151978: contig of 52469 bp in length.

FEATURES Location/Qualifiers
 source 1. .151978
 /organism="Pan troglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
 /chromosome="X"
 /map="Xq28"
 /clone="RP43-015P08"
 gap 14832. .14931
 /estimated_length=unknown
 gap 33676. .33775
 /estimated_length=unknown
 gap 60589. .60688
 /estimated_length=unknown
 gap 99410. .99509
 /estimated_length=unknown

ORIGIN

Query Match 99.2%; Score 124; DB 14; Length 151978;
 Best Local Similarity 100.0%; Pred. No. 1.3e-29;
 Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AAAAACAAAAACCTTTACGTAACGTTTTTGTCTGGGAGAGAAGACTACGAAGCACATTTT 61
 |||||
 Db 129795 AAAAACAAAAACCTTTACGTAACGTTTTTGTCTGGGAGAGAAGACTACGAAGCACATTTT 129854
 Qy 62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACCTAATCCTGAGTAAGGTGGCCAC 121
 |||||
 Db 129855 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACCTAATCCTGAGTAAGGTGGCCAC 129914
 Qy 122 TTTG 125
 ||||
 Db 129915 TTTG 129918

RESULT 4

AL135783

LOCUS AL135783 175706 bp DNA linear PRI 18-MAY-2005

DEFINITION Human DNA sequence from clone RP3-527F8 on chromosome Xq25-27.1
 Contains the TNFSF5 gene for tumor necrosis factor (ligand)
 superfamily (member 5 ,hyper-IgM syndrome), a novel gene, the 3'
 end of the ARHGEF6 gene for Rac/Cdc42 guanine nucleotide exchange
 factor (GEF) 6 and a CpG island, complete sequence.

ACCESSION AL135783

VERSION AL135783.6 GI:6983480

KEYWORDS HTG; ARHGEF6; TNFSF5.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 175706)

AUTHORS Bird, C.

TITLE Direct Submission

JOURNAL Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk
Clone requests: clonerequest@sanger.ac.uk

COMMENT On Feb 16, 2000 this sequence version replaced gi:6983044.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome X, constructed by the Sanger Centre Chromosome X Mapping
Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/ChrX>
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: vega@sanger.ac.uk

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one subclone; and the assembly was confirmed by restriction digest,
except on the rare occasion of the clone being a YAC.
RP3-527F8 is from the library RPCI-3 constructed by the group of
Pieter de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>
VECTOR: pCYPAC2.

FEATURES

source	Location/Qualifiers 1. .175706 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /map="q25-27.1" /clone="RP3-527F8" /clone_lib="RPCI-3"
gene	39996. .42685 /locus_tag="RP3-527F8.2-001"
mRNA	join(39996. .40060,41030. .42685) /locus_tag="RP3-527F8.2-001" /product="novel protein"
CDS	/note="match: cDNAs: BC042469.1" 41116. .41343 /locus_tag="RP3-527F8.2-001" /standard_name="OTTHUMP00000024129" /codon_start=1 /product="novel protein" /protein_id="CAI42900.1" /db_xref="GI:57208602" /db_xref="UniProt/TREMBL:Q5JVP7" /translation="MSSSLWVLPHASSCTWNVFFPDPENSFRASSSRKSSLSLSPHP"

polyA_signal HSFCMLPKSPALLYCGCLPSALWSTLAFVSP"
 42663. .42668
 /locus_tag="RP3-527F8.2-001"
 polyA_site 42685
 /locus_tag="RP3-527F8.2-001"
 gene join(48449. .48660,50522. .50653,54629. .54686,56612. .56674,
 59295. .60646)
 /gene="CD40LG"
 /locus_tag="RP3-527F8.3-001"
 mRNA join(48449. .48660,50522. .50653,54629. .54686,56612. .56674,
 59295. .60646)
 /gene="CD40LG"
 /locus_tag="RP3-527F8.3-001"
 /product="CD40 ligand (TNF superfamily, member 5,
 hyper-IgM syndrome)"
 /note="match: cDNAs: AF344841.1 AF344844.1 AF344859.1
 AF344860.1 L07414.1 X67878.1 X68550.1 X96710.1 Z15017.1"
 gene join(48483. .48660,50522. .50653,54629. .54686,59295. .60646)
 /gene="CD40LG"
 /locus_tag="RP3-527F8.3-002"
 mRNA join(48483. .48660,50522. .50653,54629. .54686,59295. .60646)
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 /locus_tag="RP3-527F8.3-002"
 /product="CD40 ligand (TNF superfamily, member 5,
 hyper-IgM syndrome)"
 /note="match: cDNAs: AF344853.1"
 CDS join(48505. .48660,50522. .50653,54629. .54686,56612. .56674,
 59295. .59671)
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 /standard_name="OTTHUMP00000024130"
 /note="match: proteins: P29965 P51749 Q9BDC7"
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 hyper-IgM syndrome)"
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 /db_xref="InterPro:IPR006052"
 /db_xref="InterPro:IPR008983"
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 EETKKENSFEMQKGDQNPQIAAHVISEASSKTTSVLQWAEKGYTMSNNLVTLENGKQ
 LTVKRQGLYYIYAQVTFCSNREASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPC
 GQQSIHLGGVFELQPGASVFVNVTDPQVSHGTGFTSFGLLKL"
 CDS join(48505. .48660,50522. .50653,54629. .54686,59295. .59671)
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 /locus_tag="RP3-527F8.3-002"
 /standard_name="OTTHUMP00000024131"
 /note="match: proteins: Q9BDM7"
 /codon_start=1
 /product="CD40 ligand (TNF superfamily, member 5,
 hyper-IgM syndrome)"
 /protein_id="CAI42902.1"
 /db_xref="GI:57208604"
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 NVTDPQVSHGTGFTSFGLLKL"


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polyA_signal 60626. 60631
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              /locus_tag="RP3-527F8.3-002"
polyA_site   60646
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              /locus_tag="RP3-527F8.3-002"
gene         complement(join(65803. 68425,69738. 69792,72276. 72375,
75263. 75352,76880. 76973,78192. 78212,79791. 79916,
80987. 81132,82146. 82224,83014. 83100,85933. 86079,
88188. 88247,90866. 91004,107164. 107286,108931. 109026,
113532. 113626,132358. 132428,143841. 144042,
145479. 145603,147764. 147848,168669. 168883))
              /gene="ARHGEF6"
              /locus_tag="RP3-527F8.4-002"
mRNA         complement(join(65803. 68425,69738. 69792,72276. 72375,
75263. 75352,76880. 76973,78192. 78212,79791. 79916,
80987. 81132,82146. 82224,83014. 83100,85933. 86079,
88188. 88247,90866. 91004,107164. 107286,108931. 109026,
113532. 113626,132358. 132428,143841. 144042,
145479. 145603,147764. 147848,168669. 168883))
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              /locus_tag="RP3-527F8.4-002"
              /product="Rac/Cdc42 guanine nucleotide exchange factor
              (GEF) 6"
              /note="match: cDNAs: BC043505.1"
gene         complement(join(65803. 68425,69738. 69792,72276. 72375,
75263. 75352,76880. 76973,78192. 78212,79791. 79916,
80987. 81132,82146. 82224,83014. 83100,85933. 86079,
88188. 88247,90866. 91004,107164. 107286,108931. 109026,
113532. 113626,132358. 132428,143841. 144042,
145479. 145603,147764. 147848,167400. 167599))
              /gene="ARHGEF6"
              /locus_tag="RP3-527F8.4-003"
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75263. 75352,76880. 76973,78192. 78212,79791. 79916,
80987. 81132,82146. 82224,83014. 83100,85933. 86079,
88188. 88247,90866. 91004,107164. 107286,108931. 109026,
113532. 113626,132358. 132428,143841. 144042,
145479. 145603,147764. 147848,167400. 167599))
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              /locus_tag="RP3-527F8.4-003"
              /product="Rac/Cdc42 guanine nucleotide exchange factor
              (GEF) 6"
              /note="match: ESTs: AU119513.1 BF791926.1 BG031451.1
              BG389231.1 BM479872.1 BM998736.1 BQ231848.1 BQ420871.1
              BU149436.1 CA405871.1"
gene         join(complement(AL683813.10:7264. 8634),
              complement(AL683813.10:5960. 6043),
              complement(147764. 147848),complement(145479. 145603),
              complement(143841. 144042),complement(132358. 132428),
              complement(113532. 113626),complement(108931. 109026),
              complement(107164. 107286),complement(90866. 91004),
              complement(88188. 88247),complement(85933. 86079),
              complement(83014. 83100),complement(82146. 82224),
              complement(80987. 81132),complement(79791. 79916),
              complement(78192. 78212),complement(76880. 76973),
              complement(75263. 75352),complement(72276. 72375),
              complement(69738. 69792),complement(65803. 68425))
              /gene="ARHGEF6"
              /locus_tag="RP3-527F8.4-001"
mRNA         join(complement(AL683813.10:7264. 8634),

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complement(AL683813.10:5960. .6043),
 complement(147764. .147848),complement(145479. .145603),
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 complement(113532. .113626),complement(108931. .109026),
 complement(107164. .107286),complement(90866. .91004),
 complement(88188. .88247),complement(85933. .86079),
 complement(83014. .83100),complement(82146. .82224),
 complement(80987. .81132),complement(79791. .79916),

Query Match 99.2%; Score 124; DB 8; Length 175706;
 Best Local Similarity 100.0%; Pred. No. 1.3e-29;
 Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AAAAACAAAAACCTTTACGTAACGTTTTTGTCTGGGAGAGAAGACTACGAAGCACATTTT 61
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 48315 AAAAACAAAAACCTTTACGTAACGTTTTTGTCTGGGAGAGAAGACTACGAAGCACATTTT 48374

Qy 62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACCTAATCCTGAGTAAGGTGGCCAC 121
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 48375 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACCTAATCCTGAGTAAGGTGGCCAC 48434

Qy 122 TTTG 125
 ||||
 Db 48435 TTTG 48438

RESULT 5

AC106521/c

LOCUS AC106521 259175 bp DNA linear HTG 08-OCT-2002
 DEFINITION Rattus norvegicus clone CH230-29H24, *** SEQUENCING IN PROGRESS
 ***, 3 unordered pieces.

ACCESSION AC106521
 VERSION AC106521.3 GI:22857484
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 259175)

AUTHORS Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
 Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
 Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
 Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
 Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
 Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
 Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
 Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
 Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
 Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
 Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
 Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
 Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
 Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
 Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
 Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
 Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
 Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
 Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
 Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
 Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,

Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
 Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
 Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
 Lorensuhewa, L., Loulseged, H., Lozado, R.J., Lu, X., Ma, J.,
 Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A.,
 Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
 Mawhiney, S., McLeod, M.P., McNeill, T.Z., Meenen, E.,
 Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
 Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L.,
 Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
 Nwaokemele, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K.,
 Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C.,
 Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L.,
 Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R.,
 Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,
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 Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,
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 Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,
 Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,
 Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K.,
 Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J.,
 Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,
 Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K.,
 Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
 Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
 Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
 Weinstock, G. and Gibbs, R.A.

TITLE	Direct Submission
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 259175)
AUTHORS	Worley, K.C.
TITLE	Direct Submission
JOURNAL	Submitted (12-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE	3 (bases 1 to 259175)
AUTHORS	Rat Genome Sequencing Consortium.
TITLE	Direct Submission
JOURNAL	Submitted (08-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT	<p>On Sep 14, 2002 this sequence version replaced gi:21731842. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.</p> <p>----- Genome Center Center: Baylor College of Medicine Center code: BCM Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu ----- Project Information</p>

Center project name: GLCE
Center clone name: CH230-29H24

----- Summary Statistics

Assembly program: Phrap; version 0.990329
Consensus quality: 236111 bases at least Q40
Consensus quality: 238370 bases at least Q30
Consensus quality: 239565 bases at least Q20
Estimated insert size: 259108; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
* NOTE: This sequence may represent more than one clone.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 254436: contig of 254436 bp in length
* 254437 254536: gap of unknown length
* 254537 256466: contig of 1930 bp in length
* 256467 256566: gap of unknown length
* 256567 259175: contig of 2609 bp in length.

FEATURES
source Location/Qualifiers
1. 259175
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-29H24"
gap 254437..254536
/estimated_length=unknown
gap 256467..256566
/estimated_length=unknown

ORIGIN

Query Match 92.0%; Score 115; DB 14; Length 259175;
Best Local Similarity 95.9%; Pred. No. 1.1e-26;
Matches 118; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 AAAACAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTTC 62
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Db 124236 AAAAGAAAAACCTTTACGTAACGTTTTTGCTGGGACAGAAGACTACGAAGCACATTTTC 124177
Qy 63 CAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAAC TAATCCTGAGTAAGGTGGCCACT 122
|||||
Db 124176 CAGGAAGTGTGGGTTGCGACGATTGTGCGCTCTTAAC TAATCCTGAGTAAGGTGGCCACT 124117
Qy 123 TTG 125
|||
Db 124116 TTG 124114

RESULT 6

AC124137

LOCUS AC124137 205673 bp DNA linear HTG 20-NOV-2002

DEFINITION Rattus norvegicus clone CH230-285J20, WORKING DRAFT SEQUENCE.

ACCESSION AC124137

VERSION AC124137.4 GI:25139769

KEYWORDS . HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLLTOP.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 205673)

AUTHORS Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
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Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hagues,M.,
Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J.,
Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C.,
Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.

TITLE Direct Submission

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 205673)

AUTHORS Worley,K.C.

TITLE Direct Submission

JOURNAL Submitted (10-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE 3 (bases 1 to 205673)

AUTHORS Rat Genome Sequencing Consortium.

TITLE Direct Submission

JOURNAL Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT On Nov 20, 2002 this sequence version replaced gi:23269442. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: KABZ

Center clone name: CH230-285J20

----- Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 192345 bases at least Q40

Consensus quality: 195056 bases at least Q30

Consensus quality: 196514 bases at least Q20

Estimated insert size: 198117; sum-of-contigs estimation

Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submitter.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 1 205673: contig of 205673 bp in length.

FEATURES Location/Qualifiers

source 1. 205673

/organism="Rattus norvegicus"

/mol_type="genomic DNA"

/db_xref="taxon:10116"

/clone="CH230-285J20"

ORIGIN

Query Match 90.7%; Score 113.4; DB 14; Length 205673;

Best Local Similarity 95.1%; Pred. No. 3.9e-26;

Matches 117; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

Qy      3 AAAACAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTTC 62
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Db      6740 AAAAGAAAAACCTTTACGTAACCTTTTTTGCTGGCACAGAAGACTACGAAGCACATTTTC 6799

Qy      63 CAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACCTAATCCTGAGTAAGGTGGCCACT 122
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Db      6800 CAGGAAGTGTGGGTTGCGACGATTGTGCGCTCTTAACCTAATCCTGAGTAAGGTGGCCACT 6859

Qy      123 TTG 125
      |||
Db      6860 TTG 6862

```

RESULT 7

```

AR350233
LOCUS      AR350233                2395 bp    DNA        linear    PAT 17-AUG-2003
DEFINITION Sequence 10 from patent US 6586245.
ACCESSION  AR350233
VERSION     AR350233.1  GI:33751204
KEYWORDS
SOURCE      Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE   1  (bases 1 to 2395)
  AUTHORS   Bennett,C.F., Baker,B.F., Wyatt,J. and Davis,S.E.
  TITLE     Antisense modulation of CD40 ligand expression
  JOURNAL    Patent: US 6586245-A 10 01-JUL-2003;
             ISIS Pharmaceuticals, Inc.; Carlsbad, CA
FEATURES
  source    Location/Qualifiers
             1. .2395
             /organism="unknown"
             /mol_type="genomic DNA"
ORIGIN

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Query Match      89.6%;  Score 112;  DB 6;  Length 2395;
Best Local Similarity  99.2%;  Pred. No. 1.4e-25;
Matches 123;  Conservative  0;  Mismatches  0;  Indels  1;  Gaps  1;

```

```

Qy      2 AAAACAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1750 AAAACAAAAACCTTTACGTAACG-TTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 1808

Qy      62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACCTAATCCTGAGTAAGGTGGCCAC 121
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1809 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACCTAATCCTGAGTAAGGTGGCCAC 1868

Qy      122 TTTG 125
      ||||
Db      1869 TTTG 1872

```

RESULT 8

```

AR629955
LOCUS      AR629955                2395 bp    DNA        linear    PAT 14-FEB-2005
DEFINITION Sequence 9 from patent US 6838556.
ACCESSION  AR629955
VERSION     AR629955.1  GI:59762089
KEYWORDS
SOURCE      Unknown.
  ORGANISM   Unknown.

```

Unclassified.

REFERENCE 1 (bases 1 to 2395)

AUTHORS Kim, J.P., Starr, D.B., Tam, A.W., Laurance, M.E., Michelotti, E.F., Velligan, M.D., Latour, D.R., Thomas, R.L., Kongpachith, A., Sheppard, L.T., Kim, M.Y. and Bruice, T.W.

TITLE Promoters for regulated gene expression

JOURNAL Patent: US 6838556-A 9 04-JAN-2005; Genelabs Technologies, Inc.; Redwood City, CA

FEATURES Location/Qualifiers

source 1..2395

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Query Match 89.6%; Score 112; DB 6; Length 2395;

Best Local Similarity 99.2%; Pred. No. 1.4e-25;

Matches 123; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 2 AAAAACAAAAACCTTTACGTAACGTTTTTGTCTGGGAGAGAAGACTACGAAGCACATTTT 61

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Qy 62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACCTAATCCTGAGTAAGGTGGCCAC 121

|||||

Db 1809 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACCTAATCCTGAGTAAGGTGGCCAC 1868

Qy 122 TTTG 125

||||

Db 1869 TTTG 1872

RESULT 9

AX351057

LOCUS AX351057 2395 bp DNA linear PAT 06-FEB-2002

DEFINITION Sequence 9 from Patent WO0194600.

ACCESSION AX351057

VERSION AX351057.1 GI:18616411

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Kim, J.P., Starr, D.B., Tam, A.W., Laurance, M.E., Michelotti, E.F., Velligan, M.D., Latour, D.R., Thomas, R.L., Kongpachith, A., Sheppard, L.T., Lim, M.Y. and Bruice, T.W.

TITLE Promoters for regulated gene expression

JOURNAL Patent: WO 0194600-A 9 13-DEC-2001; GENELABS TECHNOLOGIES, INC. (US)

FEATURES Location/Qualifiers

source 1..2395

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 89.6%; Score 112; DB 6; Length 2395;

Best Local Similarity 99.2%; Pred. No. 1.4e-25;

Matches 123; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 AAAAACAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
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 Db 1750 AAAAACAAAAACCTTTACGTAACG-TTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 1808
 QY 62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAATAATCCTGAGTAAGGTGGCCAC 121
 |||||
 Db 1809 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAATAATCCTGAGTAAGGTGGCCAC 1868
 QY 122 TTTG 125
 ||||
 Db 1869 TTTG 1872

RESULT 10

D31797

LOCUS D31797 6653 bp DNA linear PRI 23-OCT-2004

DEFINITION Homo sapiens gene for CD40 ligand, complete cds.

ACCESSION D31797 D31793 D31794 D31795 D31796

VERSION D31797.2 GI:60391277

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE 1

AUTHORS Hollenbaugh,D., Grosmaire,L.S., Kullas,C.D., Chalupny,N.J.,
 Braesch-Andersen,S., Noelle,R.J., Stamenkovic,I., Ledbetter,J.A.
 and Aruffo,A.

TITLE The human T cell antigen gp39, a member of the TNF gene family, is
 a ligand for the CD40 receptor: expression of a soluble form of
 gp39 with B cell co-stimulatory activity

JOURNAL EMBO J. 11 (12), 4313-4321 (1992)

PUBMED 1385114

REFERENCE 2

AUTHORS Spriggs,M.K., Armitage,R.J., Strockbine,L., Clifford,K.N.,
 Macduff,B.M., Sato,T.A., Maliszewski,C.R. and Fanslow,W.C.

TITLE Recombinant human CD40 ligand stimulates B cell proliferation and
 immunoglobulin E secretion

JOURNAL J. Exp. Med. 176 (6), 1543-1550 (1992)

PUBMED 1281209

REFERENCE 3

AUTHORS Villa,A., Noterengelo,L., Disanto,J., Nacchi,P., Strina,D.,
 Frattini,A., Lucchini,F., Patrosso,C., Giliani,S., Mantuano,E.,
 Agosti,S., Nocera,G., Kroczeck,R., Fischer,A., Ugazio,A., Basile,G.
 and Vezzoni,P.

TITLE Organization of the human CD40L gene: implications for molecular
 defects in X chromosome-linked hyper-IgM syndrome and prenatal
 diagnosis

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 91 (6), 2110-2114 (1994)

PUBMED 7907793

REFERENCE 4

AUTHORS Shimadzu,M., Nunoi,H., Terasaki,H., Ninomiya,R., Iwata,M.,
 Kanegasaka,S. and Matsuda,I.

TITLE Structural organization of the gene for CD40 ligand: molecular
 analysis for diagnosis of X-linked hyper-IgM syndrome

JOURNAL Biochim. Biophys. Acta 1260 (1), 67-72 (1995)

PUBMED 7999797

REFERENCE 5

AUTHORS Shimadzu,M., Terasaki,H., Ninomiya,R., Shimizu,S., Nunoi,H. and
 Matsuda,I.

TITLE Nucleotide sequence of CD40 ligand surrounding exon 5
 JOURNAL Unpublished
 REFERENCE 6 (bases 1 to 6653)
 AUTHORS Shimadzu, M.
 TITLE Direct Submission
 JOURNAL Submitted (10-JUN-1994) Mitsunobu Shimadzu, Mitsubishi Yuka
 Bio-Clinical Laboratory, Inc., Genetics; Shimura 3-30-1, Itabashi,
 Tokyo, 174, Japan (Tel:81-3-5994-2432, Fax:81-3-5994-2940)
 COMMENT On or before Mar 1, 2005 this sequence version replaced gi:662386,
 gi:664885, gi:664886, gi:662387, gi:662388.
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 protein_bind 815..819
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 protein_bind 1040..1045
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 Best Local Similarity 99.2%; Pred. No. 1.3e-25;
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Db      1869 TTTG 1872
  
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RESULT 11

AY333790

LOCUS AY333790 1878 bp mRNA linear MAM 20-JUL-2003

DEFINITION Canis familiaris CD154 (CD154) mRNA, complete cds.

ACCESSION AY333790

VERSION AY333790.1 GI:32700006

KEYWORDS

SOURCE Canis familiaris (dog)

ORGANISM Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
 Canis.

REFERENCE 1 (bases 1 to 1878)

AUTHORS Yang, S. and Sim, G.-K.

TITLE Canine CD40 and CD40 Ligand cDNA Sequences

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1878)

AUTHORS Yang, S. and Sim, G.-K.

TITLE Direct Submission

JOURNAL Submitted (01-JUL-2003) Immunology, Heska Corporation, 1613
 Prospect Parkway, Fort Collins, CO 80525, USA

FEATURES Location/Qualifiers

source

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/organism="Canis familiaris"

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gene

1..1878

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CDS

284..1066

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ORIGIN

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Best Local Similarity 97.6%; Pred. No. 7.3e-25;
Matches 122; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Qy 121 CTTTG 125
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Db 213 CTTTG 217

RESULT 12

BD211546

LOCUS BD211546 1878 bp DNA linear PAT 17-JUL-2003

DEFINITION Canine and feline immunoregulatory proteins, nucleic acid molecules and method of using the same.

ACCESSION BD211546

VERSION BD211546.1 GI:33021316

KEYWORDS JP 2002516104-A/52.

SOURCE Canis familiaris (dog)

ORGANISM Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.

REFERENCE 1 (bases 1 to 1878)

AUTHORS Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.

TITLE Canine and feline immunoregulatory proteins, nucleic acid molecules and method of using the same

JOURNAL Patent: JP 2002516104-A 52 04-JUN-2002;
HESKA CORP

COMMENT OS Canis familiaris (dog)

PN JP 2002516104-A/52

PD 04-JUN-2002

PF 28-MAY-1999 JP 2000551002

PR 29-MAY-1998 US 60/087306

PI GEKKEE SIM, SHUMIN YANG, MATTHEW J DREITZ, RAMANI S WONDERLING PC
C12N15/09, A61K31/7088, A61K38/00, A61K38/21, A61K39/00, A61K39/395,

PC A61K39/395,

PC A61K45/00, A61K48/00, A61P37/02, A61P37/04, C07K14/475, C07K14/535,

PC C07K14/54,

PC C07K14/56, C07K14/705, C07K16/24, C07K16/28, C12N1/21, C12N5/10, PC
G01N33/15,

PC G01N33/50, C12N15/00, A61K37/02, A61K37/66, C12N5/00 CC Canine
and feline immunoregulatory proteins, nucleic acid CC
molecules and

CC method of using the same

FH Key Location/Qualifiers

Db 213 CTTTG 217

RESULT 15
AR241525/c
LOCUS AR241525 1878 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 66 from patent US 6471957.
ACCESSION AR241525
VERSION AR241525.1 GI:27287234
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1878)
AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
TITLE Canine IL-4 immunoregulatory proteins and uses thereof
JOURNAL Patent: US 6471957-A 66 29-OCT-2002;
Heska Corporation; Fort Collins, CO;
EPX;
FEATURES Location/Qualifiers
source 1.1878
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ORIGIN

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Best Local Similarity 97.6%; Pred. No. 7.3e-25;
Matches 122; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Db 1786 AAAAAAAAAAACCTTTACGTAACCTTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 1727
Qy 61 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAATAATCCTGAGTAAGGTGGCCA 120
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Db 1726 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAATAATCCTGAGTAAGGTGGCCA 1667
Qy 121 CTTTG 125
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Db 1666 CTTTG 1662

Search completed: April 25, 2006, 12:35:25
Job time : 1775 secs

SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 10088319 and Search Result us-10-088-319-2_copy_331_455.rng.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10088319 and Search Result us-10-088-319-2_copy_331_455.rng.

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OM nucleic - nucleic search, using sw model

Run on: April 25, 2006, 09:28:13 ; Search time 285 Seconds
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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	9	93.6	74.9	7057	6	ABL33848	Abl33848	Human imm
	10	93.6	74.9	7057	6	ABL34594	Abl34594	Human met
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c	15	84.6	67.7	7057	6	ABL33849	Abl33849	Human imm
c	16	84.6	67.7	7057	6	ABL34595	Abl34595	Human met
c	17	84.6	67.7	7057	6	ABL70408	Abl70408	Chemical
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c	26	30.8	24.6	1493	13	ADT15110	Adt15110	Plant cDN
c	27	30.4	24.3	454	5	ABV09654	Abv09654	Human pro
c	28	30.2	24.2	1833	10	ADD48377	Add48377	Human gen
c	29	30	24.0	7005	13	ADS47818	Ads47818	Bacterial
	30	29.8	23.8	2004	7	ADZ74714	Adz74714	Arabidops
c	31	29.8	23.8	52679	11	ACN44216	Acn44216	Mouse gen
	32	29.6	23.7	130312	14	AEB39168	Aeb39168	L. pneumo
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	34	29.4	23.5	1716	4	AAF61006	Aaf61006	P. putida
	35	29.4	23.5	5771	10	ADD45213	Add45213	Rat gene
	36	29.2	23.4	474	4	ABA59013	Aba59013	Human foe
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	38	29.2	23.4	474	4	AAK32932	Aak32932	Human bon
	39	29.2	23.4	474	4	AAK07183	Aak07183	Human bra
	40	29.2	23.4	474	4	ABS32660	Abs32660	Human liv
	41	29.2	23.4	474	6	ABS07737	Abs07737	Human gen
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c	45	28.8	23.0	5332	4	ABL29632	Abl29632	Drosophil

ALIGNMENTS

RESULT 1

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 AC AAF74905;
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 DT 23-MAY-2001 (first entry)
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 DE Human altered CD40L promoter sequence (A331C) SEQ ID NO:2.
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 KW Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
 KW diagnosis; antiarthritic; antirheumatic; immunosuppressive;
 KW antiinflammatory; inflammatory disease; autoimmune disease; ds.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200119844-A1.
 XX
 PD 22-MAR-2001.
 XX
 PF 13-SEP-2000; 2000WO-US024966.
 XX
 PR 13-SEP-1999; 99US-0153625P.
 XX
 PA (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
 XX
 PI Crow MK, Li Y;
 XX
 DR WPI; 2001-244776/25.
 XX
 PT New altered CD40L promoter for use in the study, diagnosis and treatment
 PT of a variety of inflammatory disorders and autoimmune diseases, such as
 PT rheumatoid arthritis.
 XX
 PS Claim 1; Fig 2; 90pp; English.
 XX
 CC The present invention describes an isolated, purified nucleic acid, which
 CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
 CC residues 331-455 of the sequence comprising 455 nucleotides given in
 CC AAF74905 where A in the wild type sequence at position 331 (corresponding
 CC to position -125) is replaced with C. (I) has antiarthritic,
 CC antirheumatic, immunosuppressive and antiinflammatory activities, and can
 CC be used in gene therapy. (I) is useful in the study, diagnosis and
 CC treatment of inflammatory and autoimmune diseases, as well as diseases in
 CC which elevated expression of CD40L is a factor, e.g., rheumatoid
 CC arthritis. The present sequence represents the specifically claimed
 CC altered human CD40L promoter sequence; from the present invention
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 SQ Sequence 455 BP; 156 A; 72 C; 95 G; 132 T; 0 U; 0 Other;

Query Match 100.0%; Score 125; DB 4; Length 455;
 Best Local Similarity 100.0%; Pred. No. 1.9e-34;
 Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAAACAAAAACCTTTACGTAACGTTTTTGTGGGAGAGAAGACTACGAAGCACATTT 60
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 Db 331 CAAAAACAAAAACCTTTACGTAACGTTTTTGTGGGAGAGAAGACTACGAAGCACATTT 390
 QY 61 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAATAATCCTGAGTAAGGTGGCCA 120
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 QY 121 CTTTG 125

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Db 451 CTTTG 455

RESULT 2

AAF74904

ID AAF74904 standard; DNA; 455 BP.

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AC AAF74904;

XX

DT 23-MAY-2001 (first entry)

XX

DE Human wild type CD40L promoter sequence SEQ ID NO:1.

XX

KW Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;

KW diagnosis; antiarthritic; antirheumatic; immunosuppressive;

KW antiinflammatory; inflammatory disease; autoimmune disease; ds.

XX

OS Homo sapiens.

XX

PN WO200119844-A1.

XX

PD 22-MAR-2001.

XX

PF 13-SEP-2000; 2000WO-US024966.

XX

PR 13-SEP-1999; 99US-0153625P.

XX

PA (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.

XX

PI Crow MK, Li Y;

XX

DR WPI; 2001-244776/25.

XX

PT New altered CD40L promoter for use in the study, diagnosis and treatment

PT of a variety of inflammatory disorders and autoimmune diseases, such as

PT rheumatoid arthritis.

XX

PS Example 1; Fig 2; 90pp; English.

XX

CC The present invention describes an isolated, purified nucleic acid, which

CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having

CC residues 331-455 of the sequence comprising 455 nucleotides given in

CC AAF74905 where A in the wild type sequence at position 331 (corresponding

CC to position -125) is replaced with C. (I) has antiarthritic,

CC antirheumatic, immunosuppressive and antiinflammatory activities, and can

CC be used in gene therapy. (I) is useful in the study, diagnosis and

CC treatment of inflammatory and autoimmune diseases, as well as diseases in

CC which elevated expression of CD40L is a factor, e.g., rheumatoid

CC arthritis. The present sequence represents the wild type human CD40L

CC promoter sequence, which is used in an example from the present invention

XX

SQ Sequence 455 BP; 157 A; 71 C; 95 G; 132 T; 0 U; 0 Other;

Query Match 99.2%; Score 124; DB 4; Length 455;

Best Local Similarity 100.0%; Pred. No. 4.3e-34;

Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AAAAACAAAAACCTTTACGTAACGTTTTTGGCTGGGAGAGAAGACTACGAAGCACATTTT 61

|||||

Db 332 AAAAACAAAAACCTTTACGTAACGTTTTTGGCTGGGAGAGAAGACTACGAAGCACATTTT 391

Qy 62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
 |||
 Db 392 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 451
 Qy 122 TTTG 125
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 Db 452 TTTG 455

RESULT 3

ABK29860

ID ABK29860 standard; DNA; 2395 BP.

XX

AC ABK29860;

XX

DT 23-APR-2002 (first entry)

XX

DE Wild type CD40Ln D1 promoter, nucleotides -1860 to +49.

XX

KW Cyclin D1 promoter; CD40L promoter; hepatitis B virus promoter;
 KW HBV promoter; vancomycin-resistant enterococci promoter; VRE promoter;
 KW vanH promoter; androgen receptor promoter; AR promoter;
 KW human epidermal growth factor receptor 2 promoter; her2 promoter;
 KW beta lactamase promoter; Bla promoter; transgene; cancer; breast cancer;
 KW colon cancer; immunological disorder; prostate cancer; cytostatic;
 KW autoimmune disease; HBV pre-S promoter; HBV-X promoter;
 KW Enterococcus infection; immunosuppressive; antibacterial; antiviral;
 KW gene expression modulator; multiple sclerosis; MS;
 KW chronic hepatic insufficiency; cirrhosis; hepatocellular carcinoma;
 KW systematic lupus erythematosus; SLE; graft-vs-host disease; GVHD;
 KW familial adenomatous polyposis; rheumatoid arthritis; PCR; primer;
 KW transgenic; ds.

XX

OS Homo sapiens.

XX

PN WO200194600-A2.

XX

PD 13-DEC-2001.

XX

PF 06-JUN-2001; 2001WO-US018343.

XX

PR 06-JUN-2000; 2000US-0209549P.

XX

PA (GENE-) GENELABS TECHNOLOGIES INC.

XX

PI Kim JP, Starr DB, Tam AW, Laurance ME, Michelotti EF;
 PI Velligan MD, Latour DR, Thomas RL, Kongpachith A, Sheppard LT;
 PI Lim MY, Bruice TW;

XX

DR WPI; 2002-130595/17.

XX

PT New nucleic acid regulatory sequences, which are able to regulate
 PT expression of a gene operably linked to a promoter, useful for regulating
 PT the expression of transgenes and for treating e.g., cancer and
 PT immunological diseases.

XX

PS Example 2; Fig 5A-C; 95pp; English.

XX

CC The invention describes an isolated nucleic acid regulatory sequence for
 CC a cyclin D1 promoter, a CD40L promoter, vancomycin-resistant enterococci

CC (VRE) promoter, an HBV promoter, androgen receptor (AR) promoter, Human
 CC epidermal growth factor receptor 2 (HER2) promoter, or a beta lactamase
 CC (Bla) promoter. Transcription regulatory sequences may be used to
 CC regulate expression of the endogenous, autologous or heterologous genes
 CC operably linked to the promoter, and may be incorporated into
 CC heterologous nucleic acid constructs for use in regulated expression of
 CC transgenes. Regulated expression of cyclin D1 can be used in cancer
 CC therapies, such as breast, colon or pancreatic cancers and familial
 CC adenomatous polyposis. Regulation of the activity of CD40L gene promoter
 CC may be used in the treatment of immunological disorders, such as
 CC autoimmune diseases e.g. multiple sclerosis (MS), systematic lupus
 CC erythematosus (SLE), graft-vs-host disease (GVHD) and rheumatoid
 CC arthritis. Regulated expression of genes under the control of the HBV
 CC (hepatitis B)-specific core, pre-S and X promoters can be used in the
 CC therapy of HBV disease, chronic hepatic insufficiency, cirrhosis,
 CC hepatocellular carcinoma, and in the regulated expression of liver cell-
 CC specific genes. Regulated expression of the vanH gene promoter can be
 CC used in treatment of Enterococcus infection, while regulated expression
 CC of the androgen receptor gene can be used in the treatment of prostate
 CC cancer. This sequence represents the human CD40L promoter, nucleotides -
 CC 1860 to +49, the regulatory regions of which are described in the method
 CC of the invention

XX

SQ Sequence 2395 BP; 708 A; 453 C; 502 G; 732 T; 0 U; 0 Other;

Query Match 89.6%; Score 112; DB 6; Length 2395;
 Best Local Similarity 99.2%; Pred. No. 1.6e-29;
 Matches 123; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 2 AAAAACAAAAACCTTTACGTAACGTTTTTGTCTGGGAGAGAAGACTACGAAGCACATTTT 61
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1750 AAAAACAAAAACCTTTACGTAACG-TTTTGTCTGGGAGAGAAGACTACGAAGCACATTTT 1808
 Qy 62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1809 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 1868
 Qy 122 TTTG 125
 ||||
 Db 1869 TTTG 1872

RESULT 4

ACC44010

ID ACC44010 standard; DNA; 2395 BP.

XX

AC ACC44010;

XX

DT 30-MAY-2003 (first entry)

XX

DE Human CD40 ligand gene fragment #1.

XX

KW ds; cytostatic; antiinflammatory; immunomodulator; antisense; gene;

KW gene therapy; human; CD40 ligand; phosphorothioate; 2'MOE wings; cancer;

KW autoimmune disorder; inflammatory disorder; apoptosis.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1939..2094

FT /*tag= a

RESULT 5
 AAZ55534
 ID AAZ55534 standard; cDNA; 1878 BP.
 XX
 AC AAZ55534;
 XX
 DT 14-MAR-2000 (first entry)
 XX
 DE Canine CD154 cDNA.
 XX
 KW CD154; CD40 ligand; antibody; canine; feline; inhibitor; immune response;
 KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
 XX
 OS Canis familiaris.
 XX
 FH Key Location/Qualifiers
 FT CDS 284..1066
 FT /*tag= a
 FT /product= "Canine CD154"
 XX
 PN WO9961618-A2.
 XX
 PD 02-DEC-1999.
 XX
 PF 28-MAY-1999; 99WO-US011942.
 XX
 PR 29-MAY-1998; 98US-0087306P.
 XX
 PA (HESK-) HESKA CORP.
 XX
 PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
 XX
 DR WPI; 2000-072623/06.
 DR P-PSDB; AAY58215.
 XX
 PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 PT useful for treating or preventing e.g. tumors or autoimmune disease.
 XX
 PS Claim 1f; Page 205-207; 264pp; English.
 XX
 CC Sequences AAZ55533-Z55539 represent full-length or partial cDNAs encoding
 CC canine CD154 (CD40 ligand), while sequences AAZ55540-Z55545 represent
 CC feline CD154 cDNA sequences. The invention relates to canine interleukin-
 CC 4 (IL-4), canine or feline Flt-3 ligand, canine or feline CD40, canine or
 CC feline CD154, canine IL-5, canine IL-13, feline interferon-alpha (IFN-
 CC alpha) and feline granulocyte macrophage colony-stimulating factor
 CC (GM-CSF), and nucleotides which encode these immunoregulatory proteins.
 CC The proteins, their associated nucleic acids, specific antibodies and
 CC inhibitors may be used as vaccines for therapeutic or prophylactic
 CC regulation of an immune response in animals (particularly cats, dogs,
 CC horses and humans). They may be used to treat autoimmune or infectious
 CC diseases including allergies, tumours, inflammation and graft rejection,
 CC and to increase the response from a co-administered antigen. The
 CC nucleotide sequences can also be used for the recombinant production of a
 CC protein, while nucleotide fragments are useful as probes, as
 CC amplification primers and as sources of inhibitory therapeutics (e.g.,
 CC antisense oligonucleotides). The proteins may be used to raise antibodies
 CC and to screen for modulators of activity, while the antibodies may be
 CC used in detection, and in drug targetting
 XX

SQ Sequence 1878 BP; 526 A; 461 C; 434 G; 457 T; 0 U; 0 Other;

Query Match 87.8%; Score 109.8; DB 3; Length 1878;
Best Local Similarity 97.6%; Pred. No. 8.9e-29;
Matches 122; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

```
Qy      2  AAAAACAAAAAACCTTTACGTAAC-GTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 60
      ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db      93  AAAAAAAAAAACCTTTACGTAACCTTTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 152

Qy      61  TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACCTAATCCTGAGTAAGGTGGCCA 120
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db     153  TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACCTAATCCTGAGTAAGGTGGCCA 212

Qy     121  CTTTG 125
      |||||
Db     213  CTTTG 217
```

RESULT 6

AAZ55535/c

ID AAZ55535 standard; cDNA; 1878 BP.

XX

AC AAZ55535;

XX

DT 14-MAR-2000 (first entry)

XX

DE Canine CD154 cDNA complement.

XX

KW CD154; CD40 ligand; antibody; canine; feline; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

XX

OS Canis familiaris.

XX

FH	Key	Location/Qualifiers
FT	CDS	complement(813..1595)
FT		/*tag= a
FT		/product= "Canine CD154"

XX

PN WO9961618-A2.

XX

PD 02-DEC-1999.

XX

PF 28-MAY-1999; 99WO-US011942.

XX

PR 29-MAY-1998; 98US-0087306P.

XX

PA (HESK-) HESKA CORP.

XX

PI Sim G, Yang S, Dreitz MJ, Wonderling RS;

XX

DR WPI; 2000-072623/06.

DR P-PSDB; AAY58215.

XX

PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease.

XX

PS Claim 1f; Page 209-210; 264pp; English.

XX

CC Sequences AAZ55533-Z55539 represent full-length or partial cDNAs encoding
CC canine CD154 (CD40 ligand), while sequences AAZ55540-Z55545 represent

CC feline CD154 cDNA sequences. The invention relates to canine interleukin-
 CC 4 (IL-4), canine or feline Flt-3 ligand, canine or feline CD40, canine or
 CC feline CD154, canine IL-5, canine IL-13, feline interferon-alpha (IFN-
 CC alpha) and feline granulocyte macrophage colony-stimulating factor
 CC (GM-CSF), and nucleotides which encode these immunoregulatory proteins.
 CC The proteins, their associated nucleic acids, specific antibodies and
 CC inhibitors may be used as vaccines for therapeutic or prophylactic
 CC regulation of an immune response in animals (particularly cats, dogs,
 CC horses and humans). They may be used to treat autoimmune or infectious
 CC diseases including allergies, tumours, inflammation and graft rejection,
 CC and to increase the response from a co-administered antigen. The
 CC nucleotide sequences can also be used for the recombinant production of a
 CC protein, while nucleotide fragments are useful as probes, as
 CC amplification primers and as sources of inhibitory therapeutics (e.g.,
 CC antisense oligonucleotides). The proteins may be used to raise antibodies
 CC and to screen for modulators of activity, while the antibodies may be
 CC used in detection, and in drug targetting
 XX
 SQ Sequence 1878 BP; 457 A; 434 C; 461 G; 526 T; 0 U; 0 Other;

Query Match 87.8%; Score 109.8; DB 3; Length 1878;
 Best Local Similarity 97.6%; Pred. No. 8.9e-29;
 Matches 122; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 2 AAAAACAAAAACCTTTACGTAAC-GTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 60
 ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 1786 AAAAAA AAAACCTTTACGTAACCTTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 1727
 Qy 61 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACCTAATCCTGAGTAAGGTGGCCA 120
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 1726 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACCTAATCCTGAGTAAGGTGGCCA 1667
 Qy 121 CTTTG 125
 |||||
 Db 1666 CTTTG 1662

RESULT 7
 AAT05790

ID AAT05790 standard; DNA; 620 BP.
 XX
 AC AAT05790;
 XX
 DT 28-FEB-1996 (first entry)
 XX
 DE Human CD40 ligand exon 1 chromosomal DNA sequence.
 XX
 KW Exon; intron; chromosome; human CD40 ligand; PCR; amplification; primer;
 KW probe; antisense; gene therapy; HIM syndrome; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 164..319
 FT /*tag= a
 FT /product= "CD40 ligand a.a. 1-51"
 FT /note= "exon 1"
 FT intron 320..620
 FT /*tag= b
 FT /cons_splice= 5'site:No, 3'site:Yes
 FT /note= "This sequence only shows part of the 5' of the

FT intron sequence. The 3' splice site of the intron is
 FT shown in AAT05791"
 XX
 PN JP07163362-A.
 XX
 PD 27-JUN-1995.
 XX
 PF 25-NOV-1993; 93JP-00295102.
 XX
 PR 21-OCT-1993; 93JP-00263258.
 XX
 PA (MITP) MITSUBISHI YUKA BCL KK.
 XX
 DR WPI; 1995-260044/34.
 DR P-PSDB; AAR80834.
 XX
 PT Novel chromosomal DNA encoding a CD40 ligand and probes - useful for
 PT diagnosis and gene therapy of HIM syndrome.
 XX
 PS Claim 1; Page 5-6; 14pp; Japanese.
 XX
 CC The nucleotide sequence of exon 1 and surrounding 5' untranslated region
 CC and part of the 3' intron sequence from the chromosomal DNA sequence
 CC encoding the human CD40 ligand. The gene was isolated using an amplified
 CC fragment of the gene as a probe. The probe was a fragment amplified by
 CC the primers AAQ99758-9. The CD40 ligand primary gene is approx. 11 kb
 CC long and consists of 5 exons and 4 intron sequences (AAT05790-4). The
 CC sequence of the coding region was used to design a set of
 CC oligonucleotides (AAQ99760-73) which can be used as antisense probes for
 CC use in diagnosis and gene therapy of HIM syndrome
 XX
 SQ Sequence 620 BP; 158 A; 138 C; 133 G; 191 T; 0 U; 0 Other;

Query Match 77.6%; Score 97; DB 2; Length 620;
 Best Local Similarity 100.0%; Pred. No. 2.4e-24;
 Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 TTTGCTGGGAGAGAAGACTACGAAGCACATTTTCCAGGAAGTGTGGGCTGCAACGATTGT 88
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 TTTGCTGGGAGAGAAGACTACGAAGCACATTTTCCAGGAAGTGTGGGCTGCAACGATTGT 60
 Qy 89 GCGCTCTTAATAATCCTGAGTAAGGTGGCCACTTTG 125
 ||||||||||||||||||||||||||||||||||||
 Db 61 GCGCTCTTAATAATCCTGAGTAAGGTGGCCACTTTG 97

RESULT 8
 AAS46601
 ID AAS46601 standard; DNA; 7057 BP.
 XX
 AC AAS46601;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Tumour suppressor gene derived chemically modified sequence #323.
 XX
 KW Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer;
 KW tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
 KW cytosine methylation; ds.
 XX
 OS Homo sapiens.

Qy 122 TTTG 125
| | | |
Db 4970 TTTG 4973

RESULT 9

ABL33848

ID ABL33848 standard; DNA; 7057 BP.

XX

AC ABL33848;

XX

DT 26-MAR-2002 (first entry)

XX

DE Human immune system associated gene SEQ ID NO: 1821.

XX

KW Human; immune system disease; cytosine methylation; antiasthmatic;
KW antiarteriosclerotic; antianaemic; cytostatic; nootropic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
KW ds.

XX

OS Homo sapiens.

XX

PN WO200200928-A2.

XX

PD 03-JAN-2002.

XX

PF 02-JUL-2001; 2001WO-EP007537.

XX

PR 30-JUN-2000; 2000DE-01032529.

PR 01-SEP-2000; 2000DE-01043826.

XX

PA (EPIG-) EPIGENOMICS AG.

XX

PI Olek A, Piepenbrock C, Berlin K;

XX

DR WPI; 2002-130909/17.

XX

PT Nucleic acid comprising fragment of chemically modified gene, useful for
PT diagnosis and treatment of diseases associated with abnormal cytosine
PT methylation.

XX

PS Claim 1; SEQ ID NO 1821; 32pp + Sequence Listing; German.

XX

CC The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention

XX

SQ Sequence 7057 BP; 2260 A; 51 C; 1534 G; 3212 T; 0 U; 0 Other;

Query Match 74.9%; Score 93.6; DB 6; Length 7057;

Best Local Similarity 84.7%; Pred. No. 9.4e-23;

Matches 105; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 2 AAAAACAAAAACCTTTACGTAACGTTTTTGTCTGGGAGAGAAGACTACGAAGCACATTTT 61
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 4850 AAAAATAAAAAATTTTACGTAACGTTTTTGTCTGGGAGAGAAGATTACGAAGTATATTTT 4909

Qy 62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACATAATCCTGAGTAAGGTGGCCAC 121
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 4910 TTAGGAAGTGTGGGTTGTAACGATTGTGCGTTTTTAATTAATTTTGAGTAAGGTGGTTAT 4969

Qy 122 TTTG 125
 ||||
 Db 4970 TTTG 4973

RESULT 10

ABL34594

ID ABL34594 standard; DNA; 7057 BP.

XX

AC ABL34594;

XX

DT 26-MAR-2002 (first entry)

XX

DE Human metastasis associated gene SEQ ID NO: 147.

XX

KW Metastasis associated gene; cytostatic; gene therapy; cancer;

KW cytosine methylation; gene; ds.

XX

OS Homo sapiens.

XX

PN WO200177376-A2.

XX

PD 18-OCT-2001.

XX

PF 06-APR-2001; 2001WO-EP003970.

XX

PR 06-APR-2000; 2000DE-01019058.

PR 07-APR-2000; 2000DE-01019173.

PR 30-JUN-2000; 2000DE-01032529.

PR 01-SEP-2000; 2000DE-01043826.

XX

PA (EPIG-) EPIGENOMICS AG.

XX

PI Olek A, Piepenbrock C, Berlin K;

XX

DR WPI; 2002-010922/01.

XX

PT New nucleic acid derived from chemically treated metastasis genes, useful
 PT for diagnosis of cancers by analysis of cytosine methylation, also for
 PT treatment.

XX

PS Claim 1; SEQ ID NO 147; 23pp + Sequence Listing; English.

XX

CC The present invention provides a number of human metastasis associated
 CC genes which are modified by cytosine methylation. The sequences can be
 CC used in the diagnosis and treatment of cancer. The present sequence is
 CC one of the genes of the invention

XX

SQ Sequence 7057 BP; 2260 A; 51 C; 1534 G; 3212 T; 0 U; 0 Other;

Query Match 74.9%; Score 93.6; DB 6; Length 7057;

Best Local Similarity 84.7%; Pred. No. 9.4e-23;

Matches 105; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

```
Qy      2  AAAAACAAAAACCTTTACGTAACGTTTTTGTGGGAGAGAAGACTACGAAGCACATTTT 61
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      4850 AAAAATAAAAAATTTTACGTAACGTTTTTGTGGGAGAGAAGATTACGAAGTATATTTT 4909

Qy      62  CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAATAATCCTGAGTAAGGTGGCCAC 121
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      4910 TTAGGAAGTGTGGGTTGTAACGATTGTGCGTTTTTAATTAATTTGAGTAAGGTGGTTAT 4969

Qy      122 TTTG 125
      ||||
Db      4970 TTTG 4973
```

RESULT 11

ABL70407

ID ABL70407 standard; DNA; 7057 BP.

XX

AC ABL70407;

XX

DT 01-JUL-2002 (first entry)

XX

DE Chemically treated cell signalling DNA sequence#149.

XX

KW Cell signalling; cytosine methylation; cell signalling disease; cancer;
KW tumour; cytostatic; ds.

XX

OS Unidentified.

XX

PN WO200202807-A2.

XX

PD 10-JAN-2002.

XX

PF 29-JUN-2001; 2001WO-EP007471.

XX

PR 30-JUN-2000; 2000DE-01032529.

PR 01-SEP-2000; 2000DE-01043826.

XX

PA (EPIG-) EPIGENOMICS AG.

XX

PI Olek A, Piepenbrock C, Berlin K;

XX

DR WPI; 2002-154758/20.

XX

PT Nucleic acid, useful for diagnosis and therapy of diseases associated
PT with cell signaling e.g. cancer, comprises chemically modified genomic
PT sequences of genes associated with cell signaling.

XX

PS Claim 1; SEQ ID NO 297; 24pp + Sequence Listing; English.

XX

CC The invention relates to a nucleic acid comprising a sequence of at least
CC 18 bases of a segment of chemically pretreated DNA of genes associated
CC with cell signalling. The activity of the modified sequences of the
CC invention may be described as cytostatic. The object of the invention is
CC to provide the chemically modified DNA of genes associated with cell
CC signalling, as well as oligonucleotides and/or PNA-oligomers for
CC detecting cytosine methylations, as well as a method which is
CC particularly suitable for the diagnosis and/or therapy of genetic and
CC epigenetic parameters of genes associated with cell signalling. The
CC chemically modified DNA provided by the invention is useful for diagnosis

CC and therapy of diseases such as solid tumours and cancer. The sequences
CC given in records ABL70111-ABL70626 represent chemically pre-treated
CC genomic DNA's of genes associated with cell signalling. Note: The
CC sequence data for this patent is not represented in the printed
CC specification, but is based on sequence information supplied by the
CC European Patent Office

XX

SQ Sequence 7057 BP; 2260 A; 51 C; 1534 G; 3212 T; 0 U; 0 Other;

Query Match 74.9%; Score 93.6; DB 6; Length 7057;
Best Local Similarity 84.7%; Pred. No. 9.4e-23;
Matches 105; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 2 AAAAACAAAAACCTTTACGTAACGTTTTTGTGGGAGAGAAGACTACGAAGCACATTTT 61
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 4850 AAAAATAAAAAATTTTACGTAACGTTTTTGTGGGAGAGAAGATTACGAAGTATATTTT 4909

Qy 62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACATAATCCTGAGTAAGGTGGCCAC 121
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 4910 TTAGGAAGTGTGGGTTGTAACGATTGTGCGTTTTTAATTAATTTTGAGTAAGGTGGTTAT 4969

Qy 122 TTTG 125
| | | |
Db 4970 TTTG 4973

RESULT 12

AAS61354

ID AAS61354 standard; DNA; 7057 BP.

XX

AC AAS61354;

XX

DT 29-JAN-2002 (first entry)

XX

DE Human gene regulation-associated gene oligonucleotide #309.

XX

KW Human; Gene regulation-associated gene; severe combined immunodeficiency;
KW cardiac damage; inflammatory response; Haemophilia; Werner syndrome;
KW asthma; HDR syndrome; congenital heart defect; Saethre-Chotzen syndrome;
KW renal disease; Preeclampsia; cardiac allograft vascular disease;
KW colorectal cancer; thyroid cancer; oesophageal cancer; ds; tumour;
KW immunostimulant; cardiant; antiinflammatory; coagulant; antiasthmatic;
KW nephrotropic; gynecological; anti-tumour; immunosuppressive; cytostatic.

XX

OS Homo sapiens:

XX

PN WO200177375-A2.

XX

PD 18-OCT-2001.

XX

PF 06-APR-2001; 2001WO-EP003968.

XX

PR 06-APR-2000; 2000DE-01019058.

PR 07-APR-2000; 2000DE-01019173.

PR 30-JUN-2000; 2000DE-01032529.

PR 01-SEP-2000; 2000DE-01043826.

XX

PA (EPIG-) EPIGENOMICS AG.

XX

PI Olek A, Piepenbrock C, Berlin K;

XX

DR WPI; 2002-017470/02.

XX

PT New nucleic acid sequences from chemically modified genes associated with
PT gene regulation, useful for analyzing cytosine methylations for diagnosis
PT and therapy of diseases e.g. severe combined immunodeficiency disease.

XX

PS Disclosure; SEQ ID NO 317; 26pp; English.

XX

CC The invention relates to 224 nucleic acid sequences comprising at least
CC 18 bases of a chemically pretreated gene associated with gene regulation
CC selected from 43 known genes (or complementary sequences). The chemical
CC pretreatment converts cytosine bases unmethylated at the 5-position to
CC uracil or another base with hybridisation behaviour dissimilar to
CC cytosine, to enable analysis of cytosine methylations. The DNA sequences,
CC oligomers (or sets/arrays) and method are useful in the diagnosis of
CC diseases (or predisposition to diseases) associated with gene regulation
CC and in therapy of such diseases, by enabling analysis of the cytosine
CC methylation patterns of such genes, kits are provided. They are
CC especially useful in diagnosis and therapy of e.g. severe combined
CC immunodeficiency disease, cardiac disorders, haemophilia, solid tumours
CC and cancer, Werner syndrome, asthma, HDR syndrome, Saethre-Chotzen
CC syndrome, renal disease, preeclampsia, graft versus-host disease. The
CC present sequence is a sequence included in the sequence data for this
CC specification and is associated with the human gene regulation-associated
CC genes. Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 7057 BP; 2260 A; 51 C; 1534 G; 3212 T; 0 U; 0 Other;

Query Match 74.9%; Score 93.6; DB 6; Length 7057;
Best Local Similarity 84.7%; Pred. No. 9.4e-23;
Matches 105; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 2 AAAAACAAAAACCTTTACGTAACGTTTTTGTCTGGGAGAGAAGACTACGAAGCACATTTT 61
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 4850 AAAAATAAAAAATTTTACGTAACGTTTTTGTCTGGGAGAGAAGATTACGAAGTATATTTT 4909

Qy 62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 4910 TTAGGAAGTGTGGGTTGTAACGATTGTGCGTTTTTAATTAATTTTGAGTAAGGTGGTTAT 4969

Qy 122 TTTG 125
| | | |
Db 4970 TTTG 4973

RESULT 13

ADS99855

ID ADS99855 standard; DNA; 7057 BP.

XX

AC ADS99855;

XX

DT 02-DEC-2004 (first entry)

XX

DE Bisulphite treated human gene associated with metastasis #74.

XX

KW Human; ds; gene; Bisulphite; metastasis; cancer; cytostatic;

KW DNA methylation; matrix-assisted laser desorption/ionisation; MALDI;

KW electrospray; mass spectrometry; CpG dinucleotide; solid tumour.

XX

OS Homo sapiens.
 XX
 PN US2003148327-A1.
 XX
 PD 07-AUG-2003.
 XX
 PF 21-JAN-2003; 2003US-00240485.
 XX
 PR 06-APR-2000; 2000DE-01019058.
 PR 07-APR-2000; 2000DE-01019173.
 PR 30-JUN-2000; 2000DE-01032529.
 PR 01-SEP-2000; 2000DE-01043826.
 PR 06-APR-2001; 2001WO-EP003970.
 XX
 PA (OLEK/) OLEK A.
 PA (PIEP/) PIEPENBROCK C.
 PA (BERL/) BERLIN K.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2002-010922/01.
 XX
 PT New nucleic acid derived from chemically treated metastasis genes, useful
 PT for diagnosis of cancers by analysis of cytosine methylation, also for
 PT treatment.
 XX
 PS Claim 1; SEQ ID NO 147; 9pp; English.
 XX
 CC The invention relates to a nucleic acid comprising at least 18 bases from
 CC a segment of the chemically pretreated DNA of genes associated with
 CC metastasis, i.e. any of ADS99709-ADS99906 human genomic sequences or any
 CC of the 19 sequences appearing as ADS99911-ADS99929. SEQ ID 2,4,6 etc are
 CC the complements of SEQ ID 1,3,5, etc. Also included are an oligomer
 CC (particularly an oligonucleotide or peptide nucleic acid) comprising at
 CC least one base sequence of at least 9 bases which hybridises to (or is
 CC identical with) the sequences referred to above, producing an array of
 CC the oligomers on a carrier, obtaining genetic and/or epigenetic
 CC parameters for diagnosis and/or therapy of diseases (or predisposition to
 CC them) by analysis of cytosine methylation and a kit comprising a
 CC bisulphite (disulphite or hydrogen sulphite) and the oligomers. In the
 CC method of above 5-unmethylated cytosines in a genomic DNA sample are
 CC converted chemically to uracil, or another base with hybridisation
 CC properties different from those of cytosine, then fragments of the
 CC treated DNA amplified (particularly by polymerase chain reaction) using
 CC the oligomers and a polymerase (preferably heat stable) to produce
 CC labelled amplicons. These are tested for hybridisation to an array of
 CC oligomers and any hybridisation detected. The amplicons are labelled with
 CC fluorescent or radioactive markers, or with a detachable mass marker to
 CC allow their detection by mass spectrometry, specifically using the matrix
 CC -assisted laser desorption/ionisation (MALDI) or electrospray techniques.
 CC To improve detection in the mass spectrometer, fragments formed in the
 CC instrument have only a single net charge (positive or negative). The
 CC genomic DNA is from e.g. a cell line, biopsy sample, blood, or paraffin-
 CC embedded tissue sample. Oligonucleotides or peptide-nucleic acids that
 CC are complementary to (or identical with) parts of the nuclei acids listed
 CC above may be used as primers for amplification of the nucleic acids or
 CC their complements, and for determining cytosine methylation status and/or
 CC single nucleotide polymorphisms in metastasis-related genes. They can be
 CC used for analysis of diseases associated with methylation of CpG
 CC dinucleotides and to determine (epi)genetic parameters for diagnosis
 CC and/or therapy of disease (or predisposition). The genomic DNA sequences

PT diseases associated with cytosine methylation state e.g. cancer.
 XX
 PS Claim 1; SEQ ID NO 324; 27pp; English.
 XX
 CC The invention relates to a nucleic acid comprising a sequence of 18
 CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with
 CC bisulphite, of genes associated with tumour suppression and oncogenes
 CC having a sequence taken from 536 (actually 533 since numbers 408, 458 and
 CC 500 are missing from the sequence listing) sequences (Ss) and sequences
 CC complementary to (Ss). The nucleic acid may be a peptide nucleic acid-
 CC oligomer (PNA) of at least 9 nucleotides and may form part of a set of
 CC probes for detecting the cytosine methylation state and/or single
 CC nucleotide polymorphisms and also to be used in an array for analysing
 CC diseases associated with CpG dinucleotides e.g. cancers and tumours. The
 CC probes can also be used in a method for ascertaining genetic and/or
 CC epigenetic parameters for the diagnosis and/or therapy of existing
 CC diseases or the predisposition to specific diseases, by analysing
 CC cytosine methylations. The parameters may be compared to another set of
 CC genetic and/or epigenetic parameters, the differences serving as basis
 CC for diagnosis and/or prognosis events which are disadvantageous to
 CC patients. The present sequence is one of the 533 genomic sequences
 CC derived from tumour suppressor genes and oncogenes. Sequences with even
 CC numbered Seq ID numbers are the complementary sequence of the
 CC corresponding odd numbered sequence (e.g. ID 2 and ID1, ID 536 and ID
 CC 535, except for those whose partner sequence is missing). Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 7057 BP; 2004 A; 51 C; 1259 G; 3743 T; 0 U; 0 Other;

Query Match 67.7%; Score 84.6; DB 4; Length 7057;
 Best Local Similarity 80.5%; Pred. No. 1.6e-19;
 Matches 99; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

Qy 2 AAAAACAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
 ||||||||||||||||||||||||||||| || | | | ||||||| |||||||
 Db 2208 AAAAACAAAAACCTTTACGTAACGTTTTTACTAAAAAAAACCTACGAAACACATTTT 2149
 Qy 62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACCTAATCCTGAGTAAGGTGGCCAC 121
 ||| || | | ||||||| | ||||||||||| | ||| | ||||
 Db 2148 CCAAAAAATATAAACTACAACGATTATACGCTCTTAACCTAATCCTAAATAAAATAACCAC 2089
 Qy 122 TTT 124
 |||
 Db 2088 TTT 2086

RESULT 15
 ABL33849/c
 ID ABL33849 standard; DNA; 7057 BP.
 XX
 AC ABL33849;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Human immune system associated gene SEQ ID NO: 1822.
 XX
 KW Human; immune system disease; cytosine methylation; antiasthmatic;
 KW antiarteriosclerotic; antianaemic; cytostatic; nootropic;
 KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;

KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
 KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
 KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
 KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
 KW ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200200928-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 02-JUL-2001; 2001WO-EP007537.
 XX
 PR 30-JUN-2000; 2000DE-01032529.
 PR 01-SEP-2000; 2000DE-01043826.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2002-130909/17.
 XX
 PT Nucleic acid comprising fragment of chemically modified gene, useful for
 PT diagnosis and treatment of diseases associated with abnormal cytosine
 PT methylation.
 XX
 PS Claim 1; SEQ ID NO 1822; 32pp + Sequence Listing; German.
 XX
 CC The present invention provides a number of human immune system associated
 CC genes which are modified by the methylation of cytosines. The sequences
 CC can be used in the diagnosis and treatment of immune system disorders,
 CC including eye diseases such as retinopathy, neovascular glaucoma and
 CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
 CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
 CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
 CC diseases. The present sequence is a gene of the invention
 XX
 SQ Sequence 7057 BP; 2004 A; 51 C; 1259 G; 3743 T; 0 U; 0 Other;

Query Match 67.7%; Score 84.6; DB 6; Length 7057;
 Best Local Similarity 80.5%; Pred. No. 1.6e-19;
 Matches 99; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

Qy 2 AAAAACAAAAACCTTTACGTAACGTTTTTGTCTGGGAGAGAAGACTACGAAGCACATTTT 61
 |||||
 Db 2208 AAAAACAAAAACCTTTACGTAACGTTTTTACTAAAAAAAACCTACGAAACACATTTT 2149
 Qy 62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACCTAATCCTGAGTAAGGTGGCCAC 121
 ||| ||| ||| |||
 Db 2148 CCAAAAAATATAAACTACAACGATTATACGCTCTTAACCTAATCCTAAATAAAATAACCAC 2089
 Qy 122 TTT 124
 |||
 Db 2088 TTT 2086

Search completed: April 25, 2006, 10:12:51
 Job time : 287 secs

SCORE Search Results Details for Application 10088319 and Search Result us-10-088-319-2_copy_331_455.rni.

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OM nucleic - nucleic search, using sw model

Run on: April 25, 2006, 10:13:01 ; Search time 104 Seconds
(without alignments)
2136.492 Million cell updates/sec

Title: US-10-088-319-2_COPY_331_455
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query
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No.	Score	Match	Length	DB	ID	Description
1	112	89.6	2395	3	US-09-909-595-10	Sequence 10, Appl
2	112	89.6	2395	3	US-09-875-453B-9	Sequence 9, Appli
3	109.8	87.8	1878	3	US-09-322-409-64	Sequence 64, Appl
c 4	109.8	87.8	1878	3	US-09-322-409-66	Sequence 66, Appl
5	109.8	87.8	1878	3	US-09-451-527-64	Sequence 64, Appl
c 6	109.8	87.8	1878	3	US-09-451-527-66	Sequence 66, Appl
7	37	29.6	37	3	US-09-875-453B-15	Sequence 15, Appl
8	32.8	26.2	1830121	3	US-09-557-884-1	Sequence 1, Appli
9	32.8	26.2	1830121	3	US-09-643-990A-1	Sequence 1, Appli
10	32.8	26.2	1830121	3	US-10-158-865-1	Sequence 1, Appli
c 11	28.8	23.0	340380	3	US-09-949-016-14179	Sequence 14179, A
12	28.6	22.9	894	3	US-09-248-796A-1443	Sequence 1443, Ap
13	28.4	22.7	74790	3	US-09-949-016-15321	Sequence 15321, A
14	28.2	22.6	1746	3	US-09-107-532A-3181	Sequence 3181, Ap
15	28.2	22.6	126254	3	US-09-949-016-15341	Sequence 15341, A
16	28	22.4	948	3	US-09-252-991A-10169	Sequence 10169, A
17	27.8	22.2	36203	3	US-09-949-016-15430	Sequence 15430, A
18	27.6	22.1	754	3	US-09-640-211A-511	Sequence 511, App
19	27.4	21.9	385136	3	US-09-949-016-16073	Sequence 16073, A
20	27.2	21.8	601	3	US-09-949-016-132413	Sequence 132413,
c 21	27.2	21.8	2327	3	US-09-071-709-5	Sequence 5, Appli
c 22	27.2	21.8	2327	3	US-09-713-669-5	Sequence 5, Appli
23	27.2	21.8	450395	3	US-09-949-016-15473	Sequence 15473, A
c 24	27	21.6	470	3	US-09-621-976-10700	Sequence 10700, A
25	27	21.6	876	3	US-09-328-352-1291	Sequence 1291, Ap
26	27	21.6	151256	3	US-09-949-016-12674	Sequence 12674, A
27	27	21.6	151261	3	US-09-949-016-13242	Sequence 13242, A
28	26.8	21.4	700	3	US-09-735-271-1292	Sequence 1292, Ap
c 29	26.8	21.4	54550	3	US-10-327-189-42	Sequence 42, Appl
30	26.6	21.3	374	3	US-09-640-211A-1599	Sequence 1599, Ap
31	26.6	21.3	601	3	US-09-949-016-203482	Sequence 203482,
32	26.6	21.3	601	3	US-09-949-016-203483	Sequence 203483,
33	26.6	21.3	936	3	US-09-710-279-1247	Sequence 1247, Ap
34	26.6	21.3	999	3	US-09-134-001C-1195	Sequence 1195, Ap
35	26.6	21.3	1365	3	US-09-134-001C-1601	Sequence 1601, Ap
c 36	26.6	21.3	3238	3	US-09-710-279-4150	Sequence 4150, Ap
c 37	26.6	21.3	3497	3	US-09-710-279-3617	Sequence 3617, Ap
38	26.6	21.3	37565	3	US-09-949-016-15847	Sequence 15847, A
39	26.6	21.3	56976	3	US-09-949-016-17486	Sequence 17486, A
40	26.6	21.3	101674	3	US-09-949-016-12033	Sequence 12033, A
41	26.4	21.1	1382	3	US-09-270-767-15211	Sequence 15211, A
42	26.4	21.1	7885	3	US-09-555-367A-3	Sequence 3, Appli
c 43	26.4	21.1	9062	3	US-08-956-171E-85	Sequence 85, Appl
c 44	26.4	21.1	9062	3	US-08-781-986A-85	Sequence 85, Appl
45	26.4	21.1	13875	2	US-08-734-344-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-909-595-10

; Sequence 10, Application US/09909595

; Patent No. 6586245

; GENERAL INFORMATION:

; APPLICANT: C. Frank Bennett

; APPLICANT: Brenda F. Baker

; APPLICANT: Jacqueline Wyatt

; APPLICANT: Scott E. Davis


```
; TITLE OF INVENTION: ANTISENSE MODULATION OF CD40 LIGAND EXPRESSION
; FILE REFERENCE: RTS-0223
; CURRENT APPLICATION NUMBER: US/09/909,595
; CURRENT FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 10
; LENGTH: 2395
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1939)...(2094)
US-09-909-595-10
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Query Match          89.6%;  Score 112;  DB 3;  Length 2395;
Best Local Similarity 99.2%;  Pred. No. 2.2e-31;
Matches 123;  Conservative 0;  Mismatches 0;  Indels 1;  Gaps 1;
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Qy      2  AAAAACAAAAACCTTTACGTAACGTTTTTGTCTGGGAGAGAAGACTACGAAGCACATTTT 61
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Db      1750 AAAAACAAAAACCTTTACGTAACG-TTTTGTCTGGGAGAGAAGACTACGAAGCACATTTT 1808

Qy      62  CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAATAATCCTGAGTAAGGTGGCCAC 121
      |||
Db      1809 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAATAATCCTGAGTAAGGTGGCCAC 1868

Qy      122 TTTG 125
      |||
Db      1869 TTTG 1872
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RESULT 2

US-09-875-453B-9

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; Sequence 9, Application US/09875453B
; Patent No. 6838556
; GENERAL INFORMATION:
```

```
; APPLICANT: Kim, Jungsuh P.
; APPLICANT: Starr, Douglas B.
; APPLICANT: Tam, Albert W.
; APPLICANT: Laurance, Megan E.
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongpachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Bruice, Thomas W.
```

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; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 54600-8135.US00
; CURRENT APPLICATION NUMBER: US/09/875,453B
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2395
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-875-453B-9
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Query Match 89.6%; Score 112; DB 3; Length 2395;
Best Local Similarity 99.2%; Pred. No. 2.2e-31;
Matches 123; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy      2  AAAAACAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
        |||||||
Db    1750  AAAAACAAAAACCTTTACGTAACG-TTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 1808

Qy      62  CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
        |||||||
Db    1809  CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 1868

Qy      122  TTTG 125
        ||||
Db    1869  TTTG 1872
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RESULT 3

US-09-322-409-64

; Sequence 64, Application US/09322409

; Patent No. 6471957

; GENERAL INFORMATION:

; APPLICANT: Sim, Gek-Kee

; APPLICANT: Yang, Shumin

; APPLICANT: Dreitz, Matthew J.

; APPLICANT: Wonderling, Ramani S.

; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF

; FILE REFERENCE: IM-2-C1

; CURRENT APPLICATION NUMBER: US/09/322,409

; CURRENT FILING DATE: 1999-05-28

; EARLIER APPLICATION NUMBER: 60/087,306

; EARLIER FILING DATE: 1998-05-29

; NUMBER OF SEQ ID NOS: 154

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 64

; LENGTH: 1878

; TYPE: DNA

; ORGANISM: Canis familiaris

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (284)..(1063)

US-09-322-409-64

Query Match 87.8%; Score 109.8; DB 3; Length 1878;
Best Local Similarity 97.6%; Pred. No. 1.3e-30;
Matches 122; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Qy      2  AAAAACAAAAACCTTTACGTAAC-GTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 60
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Db    93  AAAAATAAAAAACCTTTACGTAAC-TTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 152

Qy      61  TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCA 120
        |||||||
Db    153  TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCA 212

Qy      121  CTTTG 125
        ||||
Db    213  CTTTG 217
```

RESULT 4

US-09-322-409-66/c

; Sequence 66, Application US/09322409

; Patent No. 6471957

; GENERAL INFORMATION:

; APPLICANT: Sim, Gek-Kee

; APPLICANT: Yang, Shumin

; APPLICANT: Dreitz, Matthew J.

; APPLICANT: Wonderling, Ramani S.

; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF

; FILE REFERENCE: IM-2-C1

; CURRENT APPLICATION NUMBER: US/09/322,409

; CURRENT FILING DATE: 1999-05-28

; EARLIER APPLICATION NUMBER: 60/087,306

; EARLIER FILING DATE: 1998-05-29

; NUMBER OF SEQ ID NOS: 154

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 66

; LENGTH: 1878

; TYPE: DNA

; ORGANISM: Canis familiaris

US-09-322-409-66

Query Match 87.8%; Score 109.8; DB 3; Length 1878;

Best Local Similarity 97.6%; Pred. No. 1.3e-30;

Matches 122; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 2 AAAAACAAAAACCTTTACGTAAC-GTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 60

|||||

Db 1786 AAAAAAAAAAACCTTTACGTAACCTTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 1727

Qy 61 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACCTGAGTAAGGTGGCCA 120

|||||

Db 1726 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACCTGAGTAAGGTGGCCA 1667

Qy 121 CTTTG 125

|||||

Db 1666 CTTTG 1662

RESULT 5

US-09-451-527-64

; Sequence 64, Application US/09451527

; Patent No. 6482403

; GENERAL INFORMATION:

; APPLICANT: Sim, Gek-Kee

; APPLICANT: Yang, Shumin

; APPLICANT: Dreitz, Matthew J.

; APPLICANT: Wonderling, Ramani S.

; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF

; FILE REFERENCE: IM-2-C2

; CURRENT APPLICATION NUMBER: US/09/451,527

; CURRENT FILING DATE: 1999-12-01

; EARLIER APPLICATION NUMBER: 09/322,409

; EARLIER FILING DATE: 1999-05-28

; EARLIER APPLICATION NUMBER: 60/087,306

; EARLIER FILING DATE: 1998-05-29

; NUMBER OF SEQ ID NOS: 174

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 1878
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (284)..(1063)
US-09-451-527-64

Query Match 87.8%; Score 109.8; DB 3; Length 1878;
Best Local Similarity 97.6%; Pred. No. 1.3e-30;
Matches 122; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Qy      2 AAAAACAAAAACCTTTACGTAAC-GTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 60
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Db      93 AAAAAAAAAAACCTTTACGTAAC-TTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 152

Qy      61 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAAC TAATCCTGAGTAAGGTGGCCA 120
        ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db      153 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAAC TAATCCTGAGTAAGGTGGCCA 212

Qy      121 CTTTG 125
        |||||
Db      213 CTTTG 217
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RESULT 6

US-09-451-527-66/c
; Sequence 66, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 1878
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-451-527-66

Query Match 87.8%; Score 109.8; DB 3; Length 1878;
Best Local Similarity 97.6%; Pred. No. 1.3e-30;
Matches 122; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

```
Qy      2 AAAAACAAAAACCTTTACGTAAC-GTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 60
        ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db      1786 AAAAAAAAAAACCTTTACGTAAC-TTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 1727
```

```

Qy      61 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAATAATCCTGAGTAAGGTGGCCA 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1726 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAATAATCCTGAGTAAGGTGGCCA 1667

Qy      121 CTTTG 125
        |||||
Db      1666 CTTTG 1662

```

RESULT 7

```

US-09-875-453B-15
; Sequence 15, Application US/09875453B
; Patent No. 6838556
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungsuh P.
; APPLICANT: Starr, Douglas B.
; APPLICANT: Tam, Albert W.
; APPLICANT: Laurance, Megan E.
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongpachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Bruice, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 54600-8135.US00
; CURRENT APPLICATION NUMBER: US/09/875,453B
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 37
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-875-453B-15

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Query Match          29.6%; Score 37; DB 3; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      47 TACGAAGCACATTTTCCAGGAAGTGTGGGCTGCAACG 83
        ||||||||||||||||||||||||||||||||||||||||
Db      1 TACGAAGCACATTTTCCAGGAAGTGTGGGCTGCAACG 37

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RESULT 8

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US-09-557-884-1
; Sequence 1, Application US/09557884
; Patent No. 6506581
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: The Nucleotide sequence of
;                     the Haemophilus influenzae Rd Genome, Fragments
;                     Thereof, and Uses Thereof
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.

```

```

; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3 1/2 inch diskette
; COMPUTER: Dell Pentium
; OPERATING SYSTEM: MS DOS v6.22
; SOFTWARE: ASCII Text
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/557,884
; FILING DATE: 25-Apr-2000
; CLASSIFICATION:
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/476,102
; FILING DATE: JUN-5-1995
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB186P3
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
;
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1830121 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1

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Query Match          26.2%; Score 32.8; DB 3; Length 1830121;
Best Local Similarity 55.2%; Pred. No. 1.1;
Matches 64; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

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Qy      3 AAAACAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTTC 62
        ||||| || | || | || | || | || | || | || | || |
Db 754880 AAAACAAAGTACTTGGCTTTATTGATGTACCTGGGCACGAAAAATTCTTATCAAATATGC 754939

Qy      63 CAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAATAATCCTGAGTAAGGTGGC 118
        | | | | | || || || || | || | || | || | || | || |
Db 754940 TGGCAGGTTTAGGTGGCGTGCATTATGCAATGTTAATTGTGGCTGCGGATGAAGGC 754995

```

RESULT 9

US-09-643-990A-1

; Sequence 1, Application US/09643990A

; Patent No. 6528289

; GENERAL INFORMATION:

; APPLICANT: Robert D. Fleischmann

; Mark D. Adams

; Owen White

; Hamilton O. Smith

; J. Craig Venter

; TITLE OF INVENTION: The Nucleotide sequence of

; the Haemophilus influenzae Rd Genome, Fragments

; Thereof, and Uses Thereof

; NUMBER OF SEQUENCES: 1

; CORRESPONDENCE ADDRESS:


```

; PRIOR APPLICATION NUMBER: US 09/557,884
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 08/476,102
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/426,787
; PRIOR FILING DATE: 1995-04-21
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1830121
;   TYPE: DNA
;   ORGANISM: Haemophilus influenzae
;   FEATURE:
;     NAME/KEY: misc_feature
;     LOCATION: (4747)..(4747)
;     OTHER INFORMATION: n equals a,t,c, or g
;     FEATURE:
;       NAME/KEY: misc_feature
;       LOCATION: (9921)..(9921)
;       OTHER INFORMATION: n equals a,t,c, or g
;       FEATURE:
;         NAME/KEY: misc_feature
;         LOCATION: (10150)..(10150)
;         OTHER INFORMATION: n equals a,t,c, or g
;         FEATURE:
;           NAME/KEY: misc_feature
;           LOCATION: (29298)..(29298)
;           OTHER INFORMATION: n equals a,t,c, or g
;           FEATURE:
;             NAME/KEY: misc_feature
;             LOCATION: (36543)..(36543)
;             OTHER INFORMATION: n equals a,t,c, or g
;             FEATURE:
;               NAME/KEY: misc_feature
;               LOCATION: (36551)..(36551)
;               OTHER INFORMATION: n equals a,t,c, or g
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;                 NAME/KEY: misc_feature
;                 LOCATION: (36636)..(36636)
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;                   NAME/KEY: misc_feature
;                   LOCATION: (40808)..(40810)
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;                   FEATURE:
;                     NAME/KEY: misc_feature
;                     LOCATION: (44416)..(44416)
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;                       NAME/KEY: misc_feature
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;                         OTHER INFORMATION: n equals a,t,c, or g
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;                           LOCATION: (45593)..(45593)
;                           OTHER INFORMATION: n equals a,t,c, or g
;                           FEATURE:

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; NAME/KEY: misc_feature
; LOCATION: (45732)..(45732)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (47036)..(47036)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (51334)..(51334)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (51602)..(51602)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (51786)..(51786)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (51805)..(51805)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (55369)..(55369)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (65309)..(65309)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (65313)..(65313)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (80024)..(80024)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (100091)..(100091)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (102696)..(102696)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (105121)..(105121)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (107248)..(107248)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (117136)..(117136)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature

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; LOCATION: (119750)..(119750)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (119924)..(119924)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (120038)..(120038)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (121344)..(121344)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (122167)..(122167)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (122336)..(122336)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (131340)..(131340)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (131360)..(131360)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (139910)..(139910)
; OTHER INFORMATION: n equals a,t,c, or g
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; NAME/KEY: misc_feature
; LOCATION: (140398)..(140398)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (142750)..(142750)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (145058)..(145058)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (145171)..(145171)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (145942)..(145942)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (147197)..(147197)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (150841)..(150841)

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; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (152500)..(152500)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
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Query Match          26.2%; Score 32.8; DB 3; Length 1830121;
Best Local Similarity 55.2%; Pred. No. 1.1;
Matches 64; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
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```
Qy      3 AAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTTC 62
        ||||| || | | | | | | | | | | | | | | | |
Db      754880 AAAACAAAGTACTTGGCTTTATTGATGTACCTGGGCACGAAAAATCTTATCAAATATGC 754939

Qy      63 CAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAATAATCCTGAGTAAGGTGGC 118
        | | | | | | | | | | | | | | | | | | | |
Db      754940 TGGCAGGTTTAGGTGGCGTGCATTATGCAATGTTAATTGTGGCTGCGGATGAAGGC 754995
```

RESULT 11

US-09-949-016-14179/c

; Sequence 14179, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 14179

; LENGTH: 340380

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(340380)

; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-14179

```
Query Match          23.0%; Score 28.8; DB 3; Length 340380;
Best Local Similarity 54.8%; Pred. No. 17;
Matches 57; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
```

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Qy      2 AAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
        ||| |||| | | | | | | | | | | | | | | | |
Db      73536 AAACACAAACAGCCCTCGGATAACCTGATGGGTGGGTGTCAGTACTCCAGGCCCTTGC 73477

Qy      62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAATAATCC 105
        ||||| || | | | | | | | | | |
Db      73476 CCAGGAAGTTCCTGCTTTCTGCCTGTGCCCTGTCCCTCTATCC 73433
```

RESULT 12

US-09-248-796A-1443

; Sequence 1443, Application US/09248796A

; Patent No. 6747137

; GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBIC

; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/248,796A

; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/096,409

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 1443

; LENGTH: 894

; TYPE: DNA

; ORGANISM: Candida albicans

US-09-248-796A-1443

Query Match 22.9%; Score 28.6; DB 3; Length 894;

Best Local Similarity 59.0%; Pred. No. 1.7;

Matches 49; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 23 AACGTTTTTGGCTGGGAGAGAAGACTACGAAGCACATTTTCCAGGAAGTGTGGGCTGCAAC 82

Db 355 AAAGTTAGACATTATATAGAAAACCTATCTAGCCAAGTCCCAAAAAGACTTGGCGATGAT 414

Qy 83 GATTGTGCGCTCTTAACCTAATCC 105

Db 415 GATAGGTCGCTCCTAGCTAAACC 437

RESULT 13

US-09-949-016-15321

; Sequence 15321, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 15321

; LENGTH: 74790

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-15321

Query Match 22.7%; Score 28.4; DB 3; Length 74790;
Best Local Similarity 56.4%; Pred. No. 13;
Matches 53; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

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Qy      6 ACAAAAACCTTTACGTAACGTTTTTCTGGGAGAGAAGACTACGAAGCACATTTTCCAG 65
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      27003 ATAATAAGTGATTAGCAAACTAGAGTTGTGAGAGAAGTCTATGAAGAATATTTTCCAG 27062

Qy      66 GAAGTGTGGGCTGCAACGATTGTGCGCTCTTAAC 99
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      27063 AGTGTTTTTGTTTTATAAATATTTTATTTTATTTTAGC 27096
```

RESULT 14

US-09-107-532A-3181

; Sequence 3181, Application US/09107532A

; Patent No. 6583275

; GENERAL INFORMATION:

; APPLICANT: Lynn A Doucette-Stamm and David Bush

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

; NUMBER OF SEQUENCES: 7310

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: GENOME THERAPEUTICS CORPORATION

; STREET: 100 Beaver Street

; CITY: Waltham

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02354

; COMPUTER READABLE FORM:

; MEDIUM TYPE: CD-ROM ISO9660

; COMPUTER: PC

; OPERATING SYSTEM:

; SOFTWARE: ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/107,532A

; FILING DATE: 30-Jun-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/085,598

; FILING DATE: 14 May 1998

; APPLICATION NUMBER: 60/051571

; FILING DATE: July 2, 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Ariniello, Pamela Deneke

; REGISTRATION NUMBER: 40,489

; REFERENCE/DOCKET NUMBER: GTC-012

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (781)893-5007

; TELEFAX: (781)893-8277

; INFORMATION FOR SEQ ID NO: 3181:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1746 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: circular

; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; ORGANISM: Enterococcus faecium

```

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...1746
; SEQUENCE DESCRIPTION: SEQ ID NO: 3181:
US-09-107-532A-3181

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```

Query Match          22.6%; Score 28.2; DB 3; Length 1746;
Best Local Similarity 54.3%; Pred. No. 3.1;
Matches 57; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

```

```

Qy      20 CGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTTCCAGGAAGTGTGGGCTGC 79
      || ||| ||| | | ||| | | || ||||| ||| ||| |
Db      658 CGAAACGGATTTCCGCAAATCAAAGAATTCTCAGAACATTTTTCAGTTCCTGTGTCGCT 717

Qy      80 AACGATTGTGCGCTCTTAATAATCCTGAGTAAGGTGGCCACTTT 124
      || | || || ||||| | || |||||
Db      718 TCGTTCTAGCAAAAGGAATTATTCTGTATGATTATGAAAACCTTT 762

```

RESULT 15

```

US-09-949-016-15341
; Sequence 15341, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15341
; LENGTH: 126254
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(126254)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15341

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Query Match          22.6%; Score 28.2; DB 3; Length 126254;
Best Local Similarity 61.6%; Pred. No. 19;
Matches 45; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

```

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Qy      1 CAAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 60
      ||||| ||||| || | ||| | | | | || ||| | ||| |
Db      122450 CAAAAACAAAAAACTGTTCTTAATGGTGTGAGTTAGAAAGAACGTTTAAAAAAATTT 122509

Qy      61 TCCAGGAAGTGTG 73
      | |||||
Db      122510 TTTTAGAAGTGTG 122522

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Search completed: April 25, 2006, 10:53:51
Job time : 107 secs

SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 10088319 and Search Result us-10-088-319-2_copy_331_455.rnpbm.

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This page gives you Search Results detail for the Application 10088319 and Search Result us-10-088-319-2_copy_331_455.rnpbm.

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OM nucleic - nucleic search, using sw model

Run on: April 25, 2006, 10:52:12 ; Search time 430 Seconds
(without alignments)
2403.889 Million cell updates/sec

Title: US-10-088-319-2_COPY_331_455
Perfect score: 125
Sequence: 1 caaaaacaaaaaacctttac.....tgagtaagggtggccactttg 125

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
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- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query Match	Length	DB	ID	Description
1	112	89.6	2395	3	US-09-875-453-9	Sequence 9, Appli
2	112	89.6	2395	3	US-09-909-595-10	Sequence 10, Appl
3	112	89.6	2395	8	US-10-484-007-10	Sequence 10, Appl
4	109.8	87.8	1878	5	US-10-218-654-64	Sequence 64, Appl
c 5	109.8	87.8	1878	5	US-10-218-654-66	Sequence 66, Appl
6	109.8	87.8	1878	6	US-10-262-439-64	Sequence 64, Appl
c 7	109.8	87.8	1878	6	US-10-262-439-66	Sequence 66, Appl
8	93.6	74.9	7057	6	US-10-311-455-1821	Sequence 1821, Ap
9	93.6	74.9	7057	6	US-10-240-485-147	Sequence 147, App
10	93.6	74.9	7057	7	US-10-221-613-317	Sequence 317, App
11	93.6	74.9	7057	7	US-10-221-714A-323	Sequence 323, App
c 12	84.6	67.7	7057	6	US-10-311-455-1822	Sequence 1822, Ap
c 13	84.6	67.7	7057	6	US-10-240-485-148	Sequence 148, App
c 14	84.6	67.7	7057	7	US-10-221-613-318	Sequence 318, App
c 15	84.6	67.7	7057	7	US-10-221-714A-324	Sequence 324, App
16	37	29.6	37	3	US-09-875-453-15	Sequence 15, Appl
17	32.8	26.2	1830121	7	US-10-329-670-1	Sequence 1, Appli
18	32.8	26.2	1830121	8	US-10-158-865-1	Sequence 1, Appli
19	32.8	26.2	1830121	9	US-10-981-687-1	Sequence 1, Appli
20	31.4	25.1	290040	8	US-10-850-591-3	Sequence 3, Appli
21	31.4	25.1	290040	8	US-10-850-586-3	Sequence 3, Appli
c 22	30.8	24.6	1493	8	US-10-739-930-436	Sequence 436, App
c 23	30.4	24.3	454	8	US-10-357-930-9645	Sequence 9645, Ap
24	30.4	24.3	541	4	US-09-925-065A-876467	Sequence 876467,
c 25	30	24.0	545	5	US-10-027-632-79040	Sequence 79040, A
c 26	30	24.0	545	5	US-10-027-632-79041	Sequence 79041, A
c 27	30	24.0	545	5	US-10-027-632-79042	Sequence 79042, A
c 28	30	24.0	545	5	US-10-027-632-79043	Sequence 79043, A
c 29	30	24.0	545	6	US-10-027-632-79040	Sequence 79040, A
c 30	30	24.0	545	6	US-10-027-632-79041	Sequence 79041, A
c 31	30	24.0	545	6	US-10-027-632-79042	Sequence 79042, A
c 32	30	24.0	545	6	US-10-027-632-79043	Sequence 79043, A
c 33	30	24.0	7005	6	US-10-369-493-26248	Sequence 26248, A
c 34	29.8	23.8	52679	5	US-10-087-192-553	Sequence 553, App
c 35	29.6	23.7	582	4	US-09-925-065A-400790	Sequence 400790,
c 36	29.6	23.7	2144	5	US-10-027-632-100413	Sequence 100413,
c 37	29.6	23.7	2144	5	US-10-027-632-103092	Sequence 103092,
c 38	29.6	23.7	2144	6	US-10-027-632-100413	Sequence 100413,
c 39	29.6	23.7	2144	6	US-10-027-632-103092	Sequence 103092,
40	29.6	23.7	2150	5	US-10-027-632-97497	Sequence 97497, A
41	29.6	23.7	2150	6	US-10-027-632-97497	Sequence 97497, A
42	29.2	23.4	474	3	US-09-864-761-11535	Sequence 11535, A
43	28.8	23.0	500	5	US-10-027-632-104434	Sequence 104434,
44	28.8	23.0	500	5	US-10-027-632-325533	Sequence 325533,
45	28.8	23.0	500	6	US-10-027-632-104434	Sequence 104434,

ALIGNMENTS

RESULT 1

US-09-875-453-9

; Sequence 9, Application US/09875453

; Publication No. US20030027320A1

; GENERAL INFORMATION:

; APPLICANT: Kim, Jungshuh P.

; APPLICANT: Starr, Douglas B.

; APPLICANT: Tam, Albert W.

```
; APPLICANT: Laurance, Megan E.
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongpachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Bruice, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 4600-0135.30
; CURRENT APPLICATION NUMBER: US/09/875,453
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2395
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-875-453-9
```

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Query Match          89.6%; Score 112; DB 3; Length 2395;
Best Local Similarity 99.2%; Pred. No. 4.7e-29;
Matches 123; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
```

```
Qy      2  AAAAACAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
          |||||||||||||||||||
Db      1750 AAAAACAAAAACCTTTACGTAACG-TTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 1808

Qy      62  CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAATAATCCTGAGTAAGGTGGCCAC 121
          |||||||||||||||||||
Db      1809 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAATAATCCTGAGTAAGGTGGCCAC 1868

Qy      122 TTTG 125
          ||||
Db      1869 TTTG 1872
```

RESULT 2

US-09-909-595-10

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; Sequence 10, Application US/09909595
; Publication No. US20030083278A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Brenda F. Baker
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Scott E. Davis
; TITLE OF INVENTION: ANTISENSE MODULATION OF CD40 LIGAND EXPRESSION
; FILE REFERENCE: RTS-0223
; CURRENT APPLICATION NUMBER: US/09/909,595
; CURRENT FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 10
; LENGTH: 2395
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1939)...(2094)
```

US-09-909-595-10

Query Match 89.6%; Score 112; DB 3; Length 2395;
Best Local Similarity 99.2%; Pred. No. 4.7e-29;
Matches 123; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```
Qy      2 AAAAACAAAAACCTTTACGTAACGTTTTTGTGGGAGAGAAGACTACGAAGCACATTTT 61
      |||
Db      1750 AAAAACAAAAACCTTTACGTAACG-TTTTGTGGGAGAGAAGACTACGAAGCACATTTT 1808

Qy      62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
      |||
Db      1809 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 1868

Qy      122 TTTG 125
      |||
Db      1869 TTTG 1872
```

RESULT 3

US-10-484-007-10

; Sequence 10, Application US/10484007
; Publication No. US20040259824A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Brenda F. Baker
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Scott E. Davis
; APPLICANT: Isis Pharmaceuticals, Inc.
; TITLE OF INVENTION: ANTISENSE MODULATION OF CD40 LIGAND EXPRESSION
; FILE REFERENCE: RTSP-0397
; CURRENT APPLICATION NUMBER: US/10/484,007
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: 09/909,595
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 10
; LENGTH: 2395
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1939)...(2094)
US-10-484-007-10

Query Match 89.6%; Score 112; DB 8; Length 2395;
Best Local Similarity 99.2%; Pred. No. 4.7e-29;
Matches 123; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```
Qy      2 AAAAACAAAAACCTTTACGTAACGTTTTTGTGGGAGAGAAGACTACGAAGCACATTTT 61
      |||
Db      1750 AAAAACAAAAACCTTTACGTAACG-TTTTGTGGGAGAGAAGACTACGAAGCACATTTT 1808

Qy      62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
      |||
Db      1809 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 1868

Qy      122 TTTG 125
      |||
Db      1869 TTTG 1872
```

RESULT 4

US-10-218-654-64

```
; Sequence 64, Application US/10218654
; Publication No. US20030099609A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/10/218,654
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 1878
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (284)..(1063)
US-10-218-654-64
```

```
Query Match          87.8%; Score 109.8; DB 5; Length 1878;
Best Local Similarity 97.6%; Pred. No. 2.6e-28;
Matches 122; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
```

```
Qy      2 AAAAACAAAAAACCTTTACGTAAC-GTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 60
        ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db      93 AAAAAAAAAAAACCTTTACGTAACCTTTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 152

Qy      61 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACCTAATCCTGAGTAAGGTGGCCA 120
        ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db      153 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACCTAATCCTGAGTAAGGTGGCCA 212

Qy      121 CTTTG 125
        |||||
Db      213 CTTTG 217
```

RESULT 5

US-10-218-654-66/c

```
; Sequence 66, Application US/10218654
; Publication No. US20030099609A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/10/218,654
; CURRENT FILING DATE: 2002-08-13
```

; PRIOR APPLICATION NUMBER: US/09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 1878
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-218-654-66

Query Match 87.8%; Score 109.8; DB 5; Length 1878;
Best Local Similarity 97.6%; Pred. No. 2.6e-28;
Matches 122; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

```
Qy      2  AAAAAACAAAAACCTTTACGTAAC-GTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 60
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1786 AAAAAACAAAAACCTTTACGTAAC-TTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 1727

Qy      61  TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACCTAATCCTGAGTAAGGTGGCCA 120
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1726 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACCTAATCCTGAGTAAGGTGGCCA 1667

Qy      121 CTTTG 125
        |||||
Db      1666 CTTTG 1662
```

RESULT 6

US-10-262-439-64

; Sequence 64, Application US/10262439
; Publication No. US20030143196A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/10/262,439
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/451,527
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 1878
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (284)..(1063)
US-10-262-439-64

Query Match 87.8%; Score 109.8; DB 6; Length 1878;

Best Local Similarity 97.6%; Pred. No. 2.6e-28;
Matches 122; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

```
Qy      2 AAAAACAAAAAACCTTTACGTAAC-GTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 60
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      93 AAAAAAAAAAACCTTTACGTAACTTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 152

Qy      61 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAATAATCCTGAGTAAGGTGGCCA 120
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      153 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAATAATCCTGAGTAAGGTGGCCA 212

Qy      121 CTTTG 125
        |||||
Db      213 CTTTG 217
```

RESULT 7

US-10-262-439-66/c

; Sequence 66, Application US/10262439

; Publication No. US20030143196A1

; GENERAL INFORMATION:

; APPLICANT: Sim, Gek-Kee

; APPLICANT: Yang, Shumin

; APPLICANT: Dreitz, Matthew J.

; APPLICANT: Wonderling, Ramani S.

; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF

; FILE REFERENCE: IM-2-C2

; CURRENT APPLICATION NUMBER: US/10/262,439

; CURRENT FILING DATE: 2002-09-30

; PRIOR APPLICATION NUMBER: US/09/451,527

; PRIOR FILING DATE: 1999-12-01

; PRIOR APPLICATION NUMBER: 09/322,409

; PRIOR FILING DATE: 1999-05-28

; PRIOR APPLICATION NUMBER: 60/087,306

; PRIOR FILING DATE: 1998-05-29

; NUMBER OF SEQ ID NOS: 174

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 66

; LENGTH: 1878

; TYPE: DNA

; ORGANISM: Canis familiaris

US-10-262-439-66

Query Match 87.8%; Score 109.8; DB 6; Length 1878;
Best Local Similarity 97.6%; Pred. No. 2.6e-28;
Matches 122; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

```
Qy      2 AAAAACAAAAAACCTTTACGTAAC-GTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 60
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1786 AAAAAAAAAAACCTTTACGTAACTTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 1727

Qy      61 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAATAATCCTGAGTAAGGTGGCCA 120
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1726 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAATAATCCTGAGTAAGGTGGCCA 1667

Qy      121 CTTTG 125
        |||||
Db      1666 CTTTG 1662
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; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 202
; SEQ ID NO 147
; LENGTH: 7057
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-485-147
```

```
Query Match          74.9%; Score 93.6; DB 6; Length 7057;
Best Local Similarity 84.7%; Pred. No. 2.5e-22;
Matches 105; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
```

```
Qy      2 AAAAACAAAAACCTTTACGTAACGTTTTTGTGGGAGAGAAGACTACGAAGCACATTTT 61
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      4850 AAAAATAAAAAATTTTACGTAACGTTTTTGTGGGAGAGAAGATTACGAAGTATATTTT 4909

Qy      62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAAC TAATCCTGAGTAAGGTGGCCAC 121
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      4910 TTAGGAAGTGTGGGTTGTAACGATTGTGCGTTTTTAATTAATTTGAGTAAGGTGGTTAT 4969

Qy      122 TTTG 125
      ||||
Db      4970 TTTG 4973
```

```
RESULT 10
US-10-221-613-317
; Sequence 317, Application US/10221613
; Publication No. US20040029123A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, ALEXander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with Cell Cycle
; FILE REFERENCE: 5013.1004
; CURRENT APPLICATION NUMBER: US/10/221,613
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: PCT/EP01/02945
; DE 10013847.00
; DE 10019058.8
; DE 10019173.8
; DE 10032529.7
; DE 10043826.1
; PRIOR FILING DATE: 2001-03-15
; 2000-03-15
; 2000-04-06
; 2000-04-07
; 2000-06-30
; 2000-09-01
; NUMBER OF SEQ ID NOS: 428
; SEQ ID NO 317
; LENGTH: 7057
; TYPE: DNA
```



```
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with
; TITLE OF INVENTION: Metastasis
; FILE REFERENCE: 5013.1007
; CURRENT APPLICATION NUMBER: US/10/240,485
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: PCT/EP01/03970
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 202
; SEQ ID NO 148
; LENGTH: 7057
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-485-148
```

```
Query Match          67.7%; Score 84.6; DB 6; Length 7057;
Best Local Similarity 80.5%; Pred. No. 4e-19;
Matches 99; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
```

```
Qy      2  AAAAACAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
          |||
Db      2208 AAAAACAAAAACCTTTACGTAACGTTTTTACTAAAAAAAACACTACGAAACACATTTT 2149

Qy      62  CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACATAATCCTGAGTAAGGTGGCCAC 121
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      2148 CAAAAAATATAAACTACAACGATTATACGCTCTTAACATAATCCTAAATAAAATAACCAC 2089

Qy      122 TTT 124
          |||
Db      2088 TTT 2086
```

```
RESULT 14
US-10-221-613-318/c
; Sequence 318, Application US/10221613
; Publication No. US20040029123A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with Cell Cycle
; FILE REFERENCE: 5013.1004
; CURRENT APPLICATION NUMBER: US/10/221,613
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: PCT/EP01/02945
; DE 10013847.00
; DE 10019058.8
; DE 10019173.8
```

```

; DE 10032529.7
; DE 10043826.1
; PRIOR FILING DATE: 2001-03-15
; 2000-03-15
; 2000-04-06
; 2000-04-07
; 2000-06-30
; 2000-09-01
; NUMBER OF SEQ ID NOS: 428
; SEQ ID NO 318
; LENGTH: 7057
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-221-613-318

```

[illegible]

```

Query Match          67.7%; Score 84.6; DB 7; Length 7057;
Best Local Similarity 80.5%; Pred. No. 4e-19;
Matches 99; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

Qy          2  AAAAACAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
             |||
Db          2208 AAAAACAAAAACCTTTACGTAACGTTTTTACTAAAAAAAACACTACGAAACACATTTT 2149

Qy          62  CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAATCCTGAGTAAGGTGGCCAC 121
             |||
Db          2148 CCAAAAAATATAAACTACAACGATTATACGCTCTTAACTAATCCTAAATAAAATAACCAC 2089

Qy          122 TTT 124
             |||
Db          2088 TTT 2086

```

SCORE 1.3 BuildDate: 12/06/2005

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- 2: /SIDS5/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 3: /SIDS5/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 4: /SIDS5/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 5: /SIDS5/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 6: /SIDS5/ptodata/1/pubpna/US09_NEW_PUB.seq1:*
- 7: /SIDS5/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 8: /SIDS5/ptodata/1/pubpna/US10_NEW_PUB.seq1:*
- 9: /SIDS5/ptodata/1/pubpna/US10_NEW_PUB.seq2:*
- 10: /SIDS5/ptodata/1/pubpna/US10_NEW_PUB.seq3:*
- 11: /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 12: /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
- 13: /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
- 14: /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq4:*
- 15: /SIDS5/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	112	89.6	6653	14	US-11-122-329-5	Sequence 5, Appli
	2	30.4	24.3	523	9	US-10-301-480-14522	Sequence 14522, A
	3	30.4	24.3	523	10	US-10-301-480-627931	Sequence 627931,
	4	30.4	24.3	525	9	US-10-301-480-14520	Sequence 14520, A
	5	30.4	24.3	525	9	US-10-301-480-14521	Sequence 14521, A
	6	30.4	24.3	525	10	US-10-301-480-627929	Sequence 627929,
	7	30.4	24.3	525	10	US-10-301-480-627930	Sequence 627930,
	8	30.4	24.3	541	6	US-09-925-065A-876467	Sequence 876467,
	9	30	24.0	525	9	US-10-301-480-14519	Sequence 14519, A
	10	30	24.0	525	10	US-10-301-480-627928	Sequence 627928,
c	11	29.6	23.7	574	10	US-10-301-480-467966	Sequence 467966,
c	12	29.6	23.7	577	10	US-10-301-480-1081375	Sequence 1081375,
c	13	29.6	23.7	582	6	US-09-925-065A-400790	Sequence 400790,
	14	28.8	23.0	92600	8	US-10-857-780-1	Sequence 1, Appli
	15	28.6	22.9	397	6	US-09-925-065A-638583	Sequence 638583,
c	16	28.6	22.9	405	9	US-10-301-480-1740	Sequence 1740, Ap
c	17	28.6	22.9	405	10	US-10-301-480-615149	Sequence 615149,
	18	28.6	22.9	3051	9	US-10-301-480-91542	Sequence 91542, A
	19	28.6	22.9	3051	9	US-10-301-480-91543	Sequence 91543, A
	20	28.6	22.9	3051	10	US-10-301-480-704951	Sequence 704951,
	21	28.6	22.9	3051	10	US-10-301-480-704952	Sequence 704952,
c	22	28.4	22.7	452	6	US-09-925-065A-360582	Sequence 360582,
c	23	28.2	22.6	470	6	US-09-925-065A-493015	Sequence 493015,
	24	28.2	22.6	581	6	US-09-925-065A-495522	Sequence 495522,
	25	28.2	22.6	581	6	US-09-925-065A-495523	Sequence 495523,
	26	28.2	22.6	599	6	US-09-925-065A-620025	Sequence 620025,
c	27	28	22.4	546	6	US-09-925-065A-833083	Sequence 833083,
c	28	28	22.4	1732	8	US-10-750-185-51775	Sequence 51775, A
c	29	28	22.4	1732	8	US-10-750-623-51775	Sequence 51775, A
	30	27.8	22.2	830	11	US-11-096-568A-29463	Sequence 29463, A
	31	27.8	22.2	947	8	US-10-750-185-60849	Sequence 60849, A
	32	27.8	22.2	947	8	US-10-750-623-60849	Sequence 60849, A
c	33	27.8	22.2	241805	8	US-10-995-561-13215	Sequence 13215, A
c	34	27.2	21.8	533	10	US-10-301-480-276541	Sequence 276541,
c	35	27.2	21.8	533	10	US-10-301-480-276543	Sequence 276543,
c	36	27.2	21.8	533	10	US-10-301-480-889950	Sequence 889950,
c	37	27.2	21.8	533	10	US-10-301-480-889952	Sequence 889952,
c	38	27.2	21.8	540	6	US-09-925-065A-186401	Sequence 186401,
c	39	27.2	21.8	540	6	US-09-925-065A-186403	Sequence 186403,
c	40	27.2	21.8	540	6	US-09-925-065A-186404	Sequence 186404,
c	41	27.2	21.8	555	10	US-10-301-480-431686	Sequence 431686,
c	42	27.2	21.8	555	10	US-10-301-480-431688	Sequence 431688,
c	43	27.2	21.8	555	10	US-10-301-480-1045095	Sequence 1045095,
c	44	27.2	21.8	555	10	US-10-301-480-1045097	Sequence 1045097,
c	45	27.2	21.8	556	6	US-09-925-065A-360583	Sequence 360583,

ALIGNMENTS

RESULT 1
US-11-122-329-5

```
; Sequence 5, Application US/11122329
; Publication No. US20060019272A1
; GENERAL INFORMATION:
; APPLICANT: Geraci, Mark
; APPLICANT: Bull, Todd
; APPLICANT: Voelkel, Norbert
; APPLICANT: Coldren, Chris
; TITLE OF INVENTION: Diagnosis of Disease and Monitoring of Therapy Using Gene
; TITLE OF INVENTION: Expression Analysis of Peripheral Blood Cells
; FILE REFERENCE: 2848-54
; CURRENT APPLICATION NUMBER: US/11/122,329
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/568,129
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 6653
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(6653)
; OTHER INFORMATION: n = a,c,t,g
US-11-122-329-5
```

```
Query Match          89.6%; Score 112; DB 14; Length 6653;
Best Local Similarity 99.2%; Pred. No. 1.2e-27;
Matches 123; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
```

```
Qy      2  AAAAACAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
      |||
Db      1750 AAAAACAAAAACCTTTACGTAACG-TTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 1808

Qy      62  CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACCTAATCCTGAGTAAGGTGGCCAC 121
      |||
Db      1809 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACCTAATCCTGAGTAAGGTGGCCAC 1868

Qy      122  TTG 125
      |||
Db      1869 TTG 1872
```

RESULT 2

```
US-10-301-480-14522
; Sequence 14522, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14522
```


; LENGTH: 523
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-14522

Query Match 24.3%; Score 30.4; DB 9; Length 523;
Best Local Similarity 55.8%; Pred. No. 3.1;
Matches 58; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Qy 2 AAAAACAAAAACCTTTACGTAACGTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
||||| ||||| ||| |||| | || || || || || || || |||||
Db 277 AAAAAAAAAAAGATTAGGTAAAATGACTGTTGAAAGGAATGAGTAAGGCACACATTTC 336

Qy 62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAATAATCC 105
| | | | ||||| | || || || || ||
Db 337 CAGGAATTAGCAAACCTGCAGCTCGAGGGCCAGCTCCACCCCTCC 380

RESULT 3

US-10-301-480-627931

; Sequence 627931, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 627931
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-627931

Query Match 24.3%; Score 30.4; DB 10; Length 523;
Best Local Similarity 55.8%; Pred. No. 3.1;
Matches 58; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Qy 2 AAAAACAAAAACCTTTACGTAACGTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
||||| ||||| ||| |||| | || || || || || || || |||||
Db 277 AAAAAAAAAAAGATTAGGTAAAATGACTGTTGAAAGGAATGAGTAAGGCACACATTTC 336

Qy 62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAATAATCC 105
| | | | ||||| | || || || || ||
Db 337 CAGGAATTAGCAAACCTGCAGCTCGAGGGCCAGCTCCACCCCTCC 380

RESULT 4

US-10-301-480-14520

; Sequence 14520, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms

```
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14520
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-14520
```

```
Query Match          24.3%; Score 30.4; DB 9; Length 525;
Best Local Similarity 55.8%; Pred. No. 3.1;
Matches 58; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
```

```
Qy      2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
        ||||| |||||   ||| |||| |  || || || | || || | |||||
Db      283 AAAAAAAAAAAAAAGATTAGGTAAAATGACTGTTGAAAGGAATGAGTAAGGCACACATTTT 342

Qy      62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACATAATCC 105
        | | | | ||||| | | | | | | | |
Db      343 CAGGAATTAGCAAACCTGCAGCTCGAGGGCCAGCTCCACCCCTCC 386
```

RESULT 5

US-10-301-480-14521

```
; Sequence 14521, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14521
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-14521
```

```
Query Match          24.3%; Score 30.4; DB 9; Length 525;
Best Local Similarity 55.8%; Pred. No. 3.1;
Matches 58; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
```

```
Qy      2 AAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTT 61
        ||||| |||||   ||| |||| |  || || || | || || | |||||
Db      283 AAAAAAAAAAAAAAGATTAGGTAAAATGACTGTTGAAAGGAATGAGTAAGGCACACATTTT 342

Qy      62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACATAATCC 105
```


US-10-301-480-627930

Query Match 24.3%; Score 30.4; DB 10; Length 525;
Best Local Similarity 55.8%; Pred. No. 3.1;
Matches 58; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

```
Qy      2  AAAAACAAAAACCTTTACGTAACGTTTTTCTGTTGGGAGAGAAGACTACGAAGCACATTTT 61
        ||||| ||||| ||| |||| | || || || | || || | |||||
Db      283  AAAAAAAAAAAGATTAGGTAAAATGACTGTTGAAAGGAATGAGTAAGGCACACATTTC 342

Qy      62  CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAATAATCC 105
        | | | | |||| | | | || || || |
Db      343  CAGGAATTAGCAAACCTGCAGCTCGAGGGCCAGCTCCACCCCTCC 386
```

RESULT 8

US-09-925-065A-876467

; Sequence 876467, Application US/09925065A

; Publication No. US20040181048A1

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single

; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

; FILE REFERENCE: 108827.135

; CURRENT APPLICATION NUMBER: US/09/925,065A

; CURRENT FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: US 60/243,096

; PRIOR FILING DATE: 2000-10-24

; PRIOR APPLICATION NUMBER: US 60/252,147

; PRIOR FILING DATE: 2000-11-20

; PRIOR APPLICATION NUMBER: US 60/250,092

; PRIOR FILING DATE: 2000-11-30

; PRIOR APPLICATION NUMBER: US 60/261,766

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/289,846

; PRIOR FILING DATE: 2001-05-09

; NUMBER OF SEQ ID NOS: 957086

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 876467

; LENGTH: 541

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-925-065A-876467

Query Match 24.3%; Score 30.4; DB 6; Length 541;
Best Local Similarity 55.8%; Pred. No. 3.1;
Matches 58; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

```
Qy      2  AAAAACAAAAACCTTTACGTAACGTTTTTCTGTTGGGAGAGAAGACTACGAAGCACATTTT 61
        ||||| ||||| ||| |||| | || || || | || || | |||||
Db      304  AAAAAAAAAAAGATTAGGTAAAATGACTGTTGAAAGGAATGAGTAAGGCACACATTTC 363

Qy      62  CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAATAATCC 105
        | | | | |||| | | | || || || |
Db      364  CAGGAATTAGCAAACCTGCAGCTCGAGGGCCAGCTCCACCCCTCC 407
```

RESULT 9

US-10-301-480-14519

; Sequence 14519, Application US/10301480

; Publication No. US20060057564A1

```
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14519
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-14519
```

```
Query Match          24.0%; Score 30; DB 9; Length 525;
Best Local Similarity 54.8%; Pred. No. 4.3;
Matches 57; Conservative 1; Mismatches 46; Indels 0; Gaps 0;
```

```
Qy      2 AAAAACAAAAACCTTTACGTAACGTTTTTGTCTGGGAGAGAAGACTACGAAGCACATTTT 61
        ||||| ||||:|   ||| |||| |   || ||   ||   || || ||   |||||
Db      283 AAAAAAAAAAAGATTAGGTAATAATGACTGTTGAAAGGAATGAGTAAGGCACACATTC 342

Qy      62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAATAATCC 105
        | | | |   |||| |   || ||   || ||   ||
Db      343 CAGGAATTAGCAAACGCTCGAGGCCAGCTCCACCCCTCC 386
```

RESULT 10

US-10-301-480-627928

; Sequence 627928, Application US/10301480

; Publication No. US20060057564A1

; GENERAL INFORMATION:

```
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 627928
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-627928
```

```
Query Match          24.0%; Score 30; DB 10; Length 525;
Best Local Similarity 54.8%; Pred. No. 4.3;
Matches 57; Conservative 1; Mismatches 46; Indels 0; Gaps 0;
```

```
Qy      2 AAAAACAAAAACCTTTACGTAACGTTTTTGTCTGGGAGAGAAGACTACGAAGCACATTTT 61
        ||||| ||||:|   ||| |||| |   || ||   ||   || || ||   |||||
```

Db 283 AAAAAAAAAAARAAGATTAGGTAAATGACTGTTGAAAGGAATGAGTAAGGCACACATTTC 342

Qy 62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAATAATCC 105

Db 343 CAGGAATTAGCAAACCTGCAGCTCGAGGGCCAGCTCCACCCCTCC 386

RESULT 11

US-10-301-480-467966/c

; Sequence 467966, Application US/10301480

; Publication No. US20060057564A1

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms

; TITLE OF INVENTION: in the Human Genome

; FILE REFERENCE: 108827.137

; CURRENT APPLICATION NUMBER: US/10/301,480

; CURRENT FILING DATE: 2002-11-21

; PRIOR APPLICATION NUMBER: US 10/215,598

; PRIOR FILING DATE: 2002-08-09

; PRIOR APPLICATION NUMBER: US 60/311,695

; PRIOR FILING DATE: 2001-08-10

; NUMBER OF SEQ ID NOS: 1226818

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 467966

; LENGTH: 574

; TYPE: DNA

; ORGANISM: Homo sapien

US-10-301-480-467966

Query Match 23.7%; Score 29.6; DB 10; Length 574;

Best Local Similarity 64.7%; Pred. No. 6;

Matches 44; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

Qy 4 AAACAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTTCC 63

Db 331 AAATTAAGAACGATAACTTAAGGTATTTGGTGAAGAAATTTCTAAGCAGCAAAGCATTC 272

Qy 64 AGGAAGTG 71

Db 271 AAGATGTG 264

RESULT 12

US-10-301-480-1081375/c

; Sequence 1081375, Application US/10301480

; Publication No. US20060057564A1

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms

; TITLE OF INVENTION: in the Human Genome

; FILE REFERENCE: 108827.137

; CURRENT APPLICATION NUMBER: US/10/301,480

; CURRENT FILING DATE: 2002-11-21

; PRIOR APPLICATION NUMBER: US 10/215,598

; PRIOR FILING DATE: 2002-08-09

; PRIOR APPLICATION NUMBER: US 60/311,695

; PRIOR FILING DATE: 2001-08-10

; NUMBER OF SEQ ID NOS: 1226818

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 1081375

; LENGTH: 577
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1081375

Query Match 23.7%; Score 29.6; DB 10; Length 577;
Best Local Similarity 64.7%; Pred. No. 6;
Matches 44; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

Qy 4 AAACAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTTCC 63
||| || ||| | || ||| || |||| ||| ||| | ||| | |||| | ||
Db 334 AAATTAAGAACGATAACTTAAGGTATTTGGTGGAAGAAATTTCTAAGCAGCAAAGCATTC 275

Qy 64 AGGAAGTG 71
| || |||
Db 274 AAGATGTG 267

RESULT 13

US-09-925-065A-400790/c
; Sequence 400790, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 400790
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-400790

Query Match 23.7%; Score 29.6; DB 6; Length 582;
Best Local Similarity 64.7%; Pred. No. 6;
Matches 44; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

Qy 4 AAACAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTTCC 63
||| || ||| | || ||| || |||| ||| ||| | ||| | |||| | ||
Db 339 AAATTAAGAACGATAACTTAAGGTATTTGGTGGAAGAAATTTCTAAGCAGCAAAGCATTC 280

Qy 64 AGGAAGTG 71
| || |||
Db 279 AAGATGTG 272

RESULT 14

US-10-857-780-1

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; Sequence 1, Application US/10857780
; Publication No. US20050272043A1
; GENERAL INFORMATION:
; APPLICANT: ROTH, RICHARD B.
; APPLICANT: BRAUN, ANDREAS
; APPLICANT: KAMMERER, STEFAN M.
; APPLICANT: NELSON, MATTHEW ROBERTS
; APPLICANT: RENELAND, RIKARD HENRY
; APPLICANT: HOYAL-WRIGHTSON, CAROLYN R.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: SEQ-4069-CP
; CURRENT APPLICATION NUMBER: US/10/857,780
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 10/723,681
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/490,234
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: 60/525,239
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 4962
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 92600
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (22393)..(22394)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (24675)..(24676)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (31942)..(31942)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (32965)..(32966)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (33724)..(33724)
; OTHER INFORMATION: n is a, c, g, or t
US-10-857-780-1
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```
Query Match          23.0%; Score 28.8; DB 8; Length 92600;
Best Local Similarity 56.2%; Pred. No. 61;
Matches 54; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
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```
Qy      1 CAAAAACAAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 60
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      3143 CCAAACAAAGAACTAAAAATAAGCATTTCGATTGTAGGGGGCGACAAGGGAGGCAC 3202

Qy      61 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTT 96
      | | | | | | | | | | | | | | | | | |
Db      3203 TCCAGGATCTGTGGACTCCCCACTTTGTTCTGTCTT 3238
```


RESULT 15
 US-09-925-065A-638583
 ; Sequence 638583, Application US/09925065A
 ; Publication No. US20040181048A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single
 ; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
 ; FILE REFERENCE: 108827.135
 ; CURRENT APPLICATION NUMBER: US/09/925,065A
 ; CURRENT FILING DATE: 2001-08-08
 ; PRIOR APPLICATION NUMBER: US 60/243,096
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: US 60/252,147
 ; PRIOR FILING DATE: 2000-11-20
 ; PRIOR APPLICATION NUMBER: US 60/250,092
 ; PRIOR FILING DATE: 2000-11-30
 ; PRIOR APPLICATION NUMBER: US 60/261,766
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/289,846
 ; PRIOR FILING DATE: 2001-05-09
 ; NUMBER OF SEQ ID NOS: 957086
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 638583
 ; LENGTH: 397
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-925-065A-638583

Query Match 22.9%; Score 28.6; DB 6; Length 397;
 Best Local Similarity 53.0%; Pred. No. 12;
 Matches 61; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

```

Qy      7 CAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTTCCAGG 66
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      84 CCAAAGATATACAAGTAACCGTAAGCACAGAAAAAACAGCATAACTAATTATTAAAG 143

Qy      67 AAGTGTGGGCTGCAACGATTGTGCGCTCTTAAC TAATCCTGAGTAAGGTGGCCAC 121
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      144 AAGTGCAAATCAAACCATGATGAGATATCACTTTACCCCTATTAGGATGGCTAC 198
  
```

Search completed: April 25, 2006, 12:06:58
 Job time : 359 secs

SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 10088319 and Search Result us-10-088-319-2_copy_331_455.rst.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10088319 and Search Result us-10-088-319-2_copy_331_455.rst.

[start](#)

[Go Back to previous page](#)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 25, 2006, 10:08:11 ; Search time 1987 Seconds
(without alignments)
2943.324 Million cell updates/sec

Title: US-10-088-319-2_COPY_331_455
Perfect score: 125
Sequence: 1 caaaaacaaaaaacctttac.....tgagtaaggtggccactttg 125

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	119.2	95.4	740	7	CK834247	CK834247 4058618 B
2	105.4	84.3	665	8	DN995162	DN995162 TC112886
3	32.8	26.2	650	6	CA339153	CA339153 NISC_lx11
c 4	31.8	25.4	578	2	BI291532	BI291532 UI-R-DM0-
5	31.6	25.3	480	10	CE391194	CE391194 tigr-gss-
c 6	31.4	25.1	788	9	BZ459393	BZ459393 BONIE51TF
c 7	31.4	25.1	1032	11	CNS05L3M	AL342283 Tetraodon
c 8	31.2	25.0	529	2	BI291766	BI291766 UI-R-DM0-
9	31.2	25.0	579	7	CF918988	CF918988 Bflor531.
c 10	31.2	25.0	627	2	BI285373	BI285373 UI-R-DB0-
c 11	31.2	25.0	630	2	BI279004	BI279004 UI-R-DB0-
c 12	31.2	25.0	655	2	BI285082	BI285082 UI-R-DB0-
13	31	24.8	669	10	CW685817	CW685817 OG_BB004
c 14	30.8	24.6	422	3	BI527837	BI527837 1024084H1
c 15	30.8	24.6	452	3	BI999848	BI999848 1031079E0
c 16	30.8	24.6	508	3	BI995666	BI995666 1031029D0
c 17	30.8	24.6	553	5	BU652076	BU652076 1112097D0
c 18	30.8	24.6	601	3	BM003194	BM003194 1031109A1
c 19	30.8	24.6	613	3	BI723641	BI723641 1031067D0
c 20	30.8	24.6	638	3	BI723640	BI723640 1031067D0
c 21	30.8	24.6	639	3	BI724908	BI724908 1031075H0
c 22	30.8	24.6	747	2	BF864016	BF864016 963048D09
c 23	30.8	24.6	801	2	BG844410	BG844410 1024006C1
c 24	30.8	24.6	1027	9	CC258992	CC258992 CH261-52F
c 25	30.8	24.6	1427	4	CNS0A2EV	BX827719 Arabidops
c 26	30.6	24.5	432	9	BZ768094	BZ768094 SALK_1397
c 27	30.6	24.5	474	6	CB407550	CB407550 IPG030C06
28	30.6	24.5	478	7	CF962820	CF962820 8997rsice
29	30.6	24.5	634	5	BU437831	BU437831 604145016
c 30	30.6	24.5	1017	3	BQ050581	BQ050581 AGENCOURT
31	30.6	24.5	1550	10	CL019408	CL019408 CH216-5D1
32	30.4	24.3	495	7	CN679199	CN679199 E0121C11-
33	30.4	24.3	552	7	CN681667	CN681667 E0153F05-
c 34	30.4	24.3	594	3	BJ017277	BJ017277 BJ017277
c 35	30.4	24.3	741	8	DR103237	DR103237 JHU027E09
c 36	30.4	24.3	866	7	CN172789	CN172789 AGENCOURT
c 37	30.2	24.2	433	9	AZ618267	AZ618267 1M0449I20
c 38	30.2	24.2	479	9	BZ720597	BZ720597 PUDAU30TB
39	30.2	24.2	738	9	BZ720601	BZ720601 PUDAU30TD
c 40	30.2	24.2	786	6	CB308629	CB308629 AGENCOURT
41	30.2	24.2	864	6	CD379455	CD379455 PTMM04624
c 42	30.2	24.2	951	7	CO028574	CO028574 EST806958
c 43	30	24.0	665	5	BU429602	BU429602 UI-HF-BN0
44	29.8	23.8	431	5	BW514275	BW514275 BW514275
c 45	29.8	23.8	496	6	CA626341	CA626341 wlln.pk01

ALIGNMENTS

RESULT 1

CK834247

LOCUS CK834247 740 bp mRNA linear EST 04-MAR-2004

DEFINITION 4058618 BARC 8BOV Bos taurus cDNA clone 8BOV_2M16 5', mRNA sequence.

ACCESSION CK834247

VERSION CK834247.1 GI:45064536
 KEYWORDS EST.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 Pecora; Bovidae; Bovinae; Bos.
 REFERENCE 1 (bases 1 to 740)
 AUTHORS Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassell,C.P. and
 Matukumalli,L.K.
 TITLE Construction and Analysis of a cDNA Library Generated From
 Intestinal Muscle and Epithelial Tissues of Holstein Cattle
 JOURNAL Unpublished (2004)
 COMMENT Contact: Richard G. Baumann
 Bovine Functional Genomics Lab
 ANRI
 BLDG 162: BARC-EAST, Beltsville, MD 20705, USA
 Tel: 3015048604
 Fax: 3015048744
 Email: rbaumann@anri.barc.usda.gov
 Single pass sequencing. Bases called and trimmed with phred
 0.000925 using options -trim_alt '' -trim_fasta. Vector identified
 by cross_match using options -minmatch 12 -minscore 12
 Plate: 2 row: M column: 16
 Seq primer: CCTATTTAGGTGACACTATAGAAC
 High quality sequence stop: 740.

FEATURES Location/Qualifiers
 source 1..740
 /organism="Bos taurus"
 /mol_type="mRNA"
 /strain="Holstein"
 /db_xref="taxon:9913"
 /clone="8BOV_2M16"
 /sex="Female"
 /tissue_type="Epithelial, Muscle"
 /dev_stage="Lactating, Neonatal"
 /lab_host="DH10B TonA"
 /clone_lib="BARC 8BOV"
 /note="Organ: Intestine; Vector: pCMVSPORT6.1; Site_1:
 NotI; Site_2: EcoRI; Normalized cow cDNA intestinal
 library in pCMVSPORT6.1, constructed from equimolar mRNA
 pools derived from 5 sources, 4 lactating intestinal, 1
 neonatal intestinal 4/5 Lactating, Proximal Duodenum,
 Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal
 Duodenum, Jejunum, Distal Ileum"

ORIGIN

Query Match 95.4%; Score 119.2; DB 7; Length 740;
 Best Local Similarity 97.6%; Pred. No. 8.5e-29;
 Matches 121; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAAAACAAAAACCTTTACGTAACGTTTTTGTCTGGGAGAGAAGACTACGAAGCACATTTT 61
 |||
 Db 102 AAAAACAAAAACCTTTACGTAACGTTTTTGTCTGGGAGAGAAGACTGCGAAGCACATTTT 161
 Qy 62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAAC TAATCCTGAGTAAGGTGGCCAC 121
 |||
 Db 162 CCAGGAAGTGTGGGCTGCGACGATTGTGCGCTCTTAAC TAATCCTGAGTAAGGTGGCCAC 221
 Qy 122 TTTG 125
 |||

RESULT 2

DN995162

LOCUS DN995162 665 bp mRNA linear EST 17-MAY-2005

DEFINITION TC112886 Human adult whole brain, large insert, pCMV expression library Homo sapiens cDNA clone TC112886 5' similar to Homo sapiens CD40 ligand (TNF superfamily, member 5, hyper-IgM syndrome) (CD40LG), mRNA sequence.

ACCESSION DN995162

VERSION DN995162.1 GI:66254993

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 665)

AUTHORS Birkett,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Liu,L., Liu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,M., Zhang,X., Jay,G. and He,W.

TITLE High-throughput cloning of full-length human cDNAs directly from cDNA libraries optimized for large and rare transcripts

JOURNAL Unpublished (2005)

COMMENT Contact: Kovacs, KF

High Throughput cDNA Cloning

OriGene Technologies, Inc. (www.origene.com)

6 Taft Court, Suite 100, Rockville, MD 20850, USA

Tel: 301 340 3188

Fax: 301 340 8606

Email: cDNA@origene.com

This EST submission is part of an on-going human full-length cloning project at OriGene Technologies, Inc.

Please contact OriGene for access.

OriGene Technologies, Inc.

6 Taft Ct. Suite 100

Rockville, MD 20850

Tel: (301) 340-3188

http://www.origene.com

Seq primer: pCMV6 5prime forward vector primer, OriGene Technologies Inc.

FEATURES Location/Qualifiers

source

1..665

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="TC112886"

/tissue_type="Whole brain"

/clone_lib="Human adult whole brain, large insert, pCMV expression library"

/note="Organ: Brain; Vector: pCMV6-XL5; Site_1: EcoR1; Site_2: Xho1/Sall compatible end ligatio; Oligo-dT primed reverse transcription optimized for large and GC rich mRNA transcripts, cDNA size selection, optimized ligation for large inserts into mammalian expression vector, random clones selected for end sequence verification of full-length genes"

ORIGIN

Query Match

84.3%; Score 105.4; DB 8; Length 665;

Best Local Similarity 99.1%; Pred. No. 3.5e-24;
Matches 106; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      19 ACGTAACGTTTTTGTGGGAGAGAAGACTACGAAGCACATTTTCCAGGAAGTGTGGGCTG 78
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      5 AGGTAACGTTTTTGTGGGAGAGAAGACTACGAAGCACATTTTCCAGGAAGTGTGGGCTG 64

Qy      79 CAACGATTGTGCGCTCTTAATAATCCTGAGTAAGGTGGCCACTTTG 125
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     65 CAACGATTGTGCGCTCTTAATAATCCTGAGTAAGGTGGCCACTTTG 111
```

RESULT 3

CA339153

LOCUS CA339153 650 bp mRNA linear EST 04-NOV-2002

DEFINITION NISC_lx11d02.y1 NCI_CGAP_Pr51 Rattus norvegicus cDNA clone

IMAGE:5621810 5', mRNA sequence.

ACCESSION CA339153

VERSION CA339153.1 GI:24557251

KEYWORDS EST.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 650)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

cDNA Library Preparation:

cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL

DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

info@image.llnl.gov

Plate: LLAM12446 row: H column: 3

Seq primer: M13RP1 reverse primer (ABI).

FEATURES Location/Qualifiers

source

1..650

/organism="Rattus norvegicus"

/mol_type="mRNA"

/db_xref="taxon:10116"

/clone="IMAGE:5621810"

/sex="male"

/tissue_type="pool of ventral and dorsolateral prostate"

/dev_stage="adult, 10 week"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NCI_CGAP_Pr51"

/note="Organ: prostate; Vector: pCMV-SPORT6.1; Site_1:

NotI; Site_2: EcoRV; Cloned unidirectionally. Primer:

Oligo dT. Pool of 2 primary libraries: NCI_CGAP_Pr46

(ventral prostate from 10 wk male, average insert size 2

kb) and NCI_CGAP_Pr47 (dorsolateral prostate from 10 wk

male, average insert size 2 kb). Constructed by

Invitrogen. Note: this is a NCI_CGAP Library."

ORIGIN

Query Match 26.2%; Score 32.8; DB 6; Length 650;
 Best Local Similarity 54.0%; Pred. No. 8.1;
 Matches 67; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

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Qy      2 AAAAACAAAAACCTTTACGTAACGTTTTTGTCTGGGAGAGAAGACTACGAAGCACATTTT 61
      ||| | | || | || ||| | || ||| || ||||| |||| |
Db      209 AAACAACAGTGACTTGTATCTAAGTCGTGTGGTGGAAGTGAAGACAGTGAAGACAATCCA 268

Qy      62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACCTAATCCTGAGTAAGGTGGCCAC 121
      ||| | | |||| | || || | | | | | || | ||
Db      269 ACAGCAGATAGAGGCTGGAAAGACCTTGTATTATTGATGTGATCTTAAGCAAAACAGCATG 328

Qy      122 TTTG 125
      |||
Db      329 TTTG 332
  
```

RESULT 4

BI291532/c

LOCUS BI291532 578 bp mRNA linear EST 19-JUL-2001

DEFINITION UI-R-DM0-cis-n-19-0-UI.s1 UI-R-DM0 Rattus norvegicus cDNA clone
 UI-R-DM0-cis-n-19-0-UI 3', mRNA sequence.

ACCESSION BI291532

VERSION BI291532.1 GI:14951161

KEYWORDS EST.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 578)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

PUBMED 8889548

COMMENT Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

The sequence contained an oligo-dT track that was present in the
 oligonucleotide that was used to prime the synthesis of first
 strand cDNA and therefore this may represent a bonafide poly A
 tail. The sequence tag present in the cDNA between the NotI site
 and the oligo-dT track served to verify it as a clone from the
 non-normalized rat prostate library cDNA Library Preparation: M.B.
 Soares Lab Clone distribution: clones will be available through
 Research Genetics (www.resgen.com) The following repetitive
 elements were found in this cDNA sequence: 1-21,

>AT_rich#Low_complexity

Seq primer: M13 Forward

POLYA=Yes.

FEATURES

source

Location/Qualifiers

1..578

/organism="Rattus norvegicus"

/mol_type="mRNA"

/strain="Sprague-Dawley"

/db_xref="taxon:10116"

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/clone="UI-R-DM0-cis-n-19-0-UI"
/dev_stage="ADULT"
/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-DM0"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-DM0
library is a non-normalized Rat Prostate library
constructed in pT3T7 PAC vector according to the procedure
described by Bonaldo, Lennon & Soares (Genome Research
Genome 6: 791-806, 1996). The oligonucleotide used to
prime first strand synthesis contained the sequence tag
CCAGG between the Not I cloning site and dT18 stretch.
TAG_TISSUE=rat prostate
TAG_LIB=UI-R-DM0
TAG_SEQ=CCAGG"

```

ORIGIN

```

Query Match          25.4%;  Score 31.8;  DB 2;  Length 578;
Best Local Similarity 53.2%;  Pred. No. 17;
Matches   66;  Conservative   0;  Mismatches   58;  Indels     0;  Gaps     0;

Qy      2  AAAAACAAAAACCTTTACGTAACGTTTTTGTCTGGGAGAGAAGACTACGAAGCACATTTT 61
      ||| | |  || | | ||| | | | | | | | | | | | | | | | | |
Db      537 AAACAACAGTGACTTGTATNTAAGTCGTGTGGTGGGAAGTGAAGACAGTGAAGACAATCCA 478

Qy      62  CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAATAATCCTGAGTAAGGTGGCCAC 121
      ||| | |  |||| | | | | | | | | | | | | | | | | | |
Db      477 ACAGCAGATAGAGGCTGGAAAGACCTTGTTATTTGATGTGATCTTAGGCCAAAACAGCATG 418

Qy      122 TTTG 125
      ||||
Db      417 TTTG 414

```

RESULT 5

```

CE391194
LOCUS      CE391194          480 bp    DNA        linear    GSS 27-SEP-2003
DEFINITION tigr-gss-dog-17000334460145 Dog Library Canis familiaris genomic,
            genomic survey sequence.
ACCESSION  CE391194
VERSION    CE391194.1  GI:36630810
KEYWORDS   GSS.
SOURCE     Canis familiaris (dog)
ORGANISM   Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE  1  (bases 1 to 480)
AUTHORS    Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
            Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
            Venter,J.C.
TITLE      The dog genome: survey sequencing and comparative analysis
JOURNAL    Science 301 (5641), 1898-1903 (2003)
PUBMED     14512627
COMMENT    Contact: Kirkness EF
            The Institute for Genomic Research
            Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
            Rockville, MD 20850, USA
            Tel: 301-838-0200
            Fax: 301-838-0208
            Email: ekirknes@tigr.org

```


Class: shotgun.

FEATURES
 source Location/Qualifiers
 1. .480
 /organism="Canis familiaris"
 /mol_type="genomic DNA"
 /strain="Standard Poodle"
 /db_xref="taxon:9615"
 /clone_lib="Dog Library"
 /note="Site_1: BstXI; Libraries were prepared from peripheral blood"

ORIGIN

Query Match 25.3%; Score 31.6; DB 10; Length 480;
 Best Local Similarity 55.5%; Pred. No. 19;
 Matches 61; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Qy 2 AAAAACAAAAACCTTTACGTAACGTTTTTCTGGGAGAGAAGACTACGAAGCACATTTT 61
 ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 7 AAATAAATAGAATCTTTAAAAAAATTTTTTTTTTTCAAGTGAAAACTTGGAAAACTTTTA 66

Qy 62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACCTAATCCTGAGTA 111
 || | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 67 CCTGACATCAGGGGCATGACAGGTTCAAATACTTAAAGACTTCTGAGAA 116

RESULT 6
 BZ459393/c

LOCUS BZ459393 788 bp DNA linear GSS 13-DEC-2002

DEFINITION BONIE51TF BO_1.6_2_KB_tot Brassica oleracea genomic clone BONIE51, genomic survey sequence.

ACCESSION BZ459393

VERSION BZ459393.1 GI:26740861

KEYWORDS GSS.

SOURCE Brassica oleracea

ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 788)

AUTHORS Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S., Utterback,T.R., Wortman,J.R., White,O.R. and Town,C.D.

TITLE Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis

JOURNAL Genome Res. 15 (4), 487-495 (2005)

PUBMED 15805490

COMMENT Other_GSSs: BONIE51TR
 Contact: Chris Town
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TF
 Class: sheared ends.

FEATURES
 source Location/Qualifiers
 1. .788
 /organism="Brassica oleracea"
 /mol_type="genomic DNA"
 /strain="TO1000DH3"
 /db_xref="taxon:3712"

/clone="BONIE51"
/clone_lib="BO_1.6_2_KB_tot"
/note="Vector: pHO51; Site_1: BstXI; 1.6-2 kb sheared
total DNA inserted into pHO51 using BstXI linkers"

ORIGIN

Query Match 25.1%; Score 31.4; DB 9; Length 788;
Best Local Similarity 61.7%; Pred. No. 25;
Matches 50; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 CAAAAACAAAAACCTTTACGTAACGTTTTGCTGGGAGAGAAGACTACGAAGCACATTT 60
|||| || ||| ||||| || || || ||||| || ||| ||||
Db 710 CAAACGCATAAATTCCTTTATGTGGAGTATTCCTATGGAGAGGTAACATTGAAGAACATCA 651

QY 61 TCCAGGAAGTGTGGGCTGCAA 81
| ||| || ||| | || ||
Db 650 TACAGCGAGGGTGAGTTGGAA 630

RESULT 7

CNS05L3M/c

LOCUS CNS05L3M 1032 bp DNA linear GSS 01-SEP-2000

DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone
051F03 of library A from Tetraodon nigroviridis, genomic survey
sequence.

ACCESSION AL342283

VERSION AL342283.1 GI:8236041

KEYWORDS GSS; genome survey sequence.

SOURCE Tetraodon nigroviridis

ORGANISM Tetraodon nigroviridis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontoidea; Tetraodontidae; Tetraodon.

REFERENCE 1

AUTHORS Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.

TITLE Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence

JOURNAL Nat. Genet. 25 (2), 235-238 (2000)

PUBMED 10835645

REFERENCE 2

AUTHORS Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C.,
Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F.,
Saurin, W., Bernot, A. and Weissenbach, J.

TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis

JOURNAL Genome Res. 10 (7), 939-949 (2000)

PUBMED 10899143

REFERENCE 3 (bases 1 to 1032)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

COMMENT This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
<http://www.genoscope.cns.fr/Tetraodon>.

FEATURES Location/Qualifiers

source 1. .1032
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="051F03"
/clone_lib="A"
/note="Genoscope sequence ID : C0AA051CC02C1
end : T7"

ORIGIN

Query Match 25.1%; Score 31.4; DB 11; Length 1032;
Best Local Similarity 51.0%; Pred. No. 27;
Matches 53; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

Qy 4 AAACAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTTCC 63
|| ||||| || || | |||| | | || | | |||||
Db 619 AAGGAAAAANCCNTATGAAGTCNTTTTTTCANGNNNGNAAAAANANNCANNNCATTTTCT 560

Qy 64 AGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAATAATCCTG 107
| ||| || || || | || | || |||
Db 559 CTGTTGTGAGAGCCTAAAAAATGTATCATGTTTAAATTNCTG 516

RESULT 8

BI291766/c

LOCUS BI291766 529 bp mRNA linear EST 19-JUL-2001

DEFINITION UI-R-DMO-cis-n-18-0-UI.s1 UI-R-DMO Rattus norvegicus cDNA clone
UI-R-DMO-cis-n-18-0-UI 3', mRNA sequence.

ACCESSION BI291766

VERSION BI291766.1 GI:14951628

KEYWORDS EST.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 529)

AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene
discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

PUBMED 8889548

COMMENT Contact: Soares, MB

Coordinated Laboratory for Computational Genomics
University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to verify it as a clone from the
non-normalized rat prostate library cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com)

Seq primer: M13 Forward

POLYA=Yes.

FEATURES Location/Qualifiers

source 1. .529

```

/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-DM0-cis-n-18-0-UI"
/dev_stage="ADULT"
/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-DM0"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-DM0
library is a non-normalized Rat Prostate library
constructed in pT3T7 PAC vector according to the procedure
described by Bonaldo, Lennon & Soares (Genome Research
Genome 6: 791-806, 1996). The oligonucleotide used to
prime first strand synthesis contained the sequence tag
CCAGG between the Not I cloning site and dT18 stretch.
TAG_TISSUE=rat prostate
TAG_LIB=UI-R-DM0
TAG_SEQ=CCAGG"

```

ORIGIN

```

Query Match      25.0%;  Score 31.2;  DB 2;  Length 529;
Best Local Similarity 53.2%;  Pred. No. 26;
Matches 66;  Conservative 0;  Mismatches 58;  Indels 0;  Gaps 0;

Qy      2  AAAAACAAAAACCTTTACGTAACGTTTTTGTCTGGGAGAGAAGACTACGAAGCACATTTT 61
      ||| | |  || | ||  |||  | || ||| || |||||  ||||  ||
Db      527 AAACAACAGTGACTTGTATCTAAGTCGTGTGGTGAAGTGAAGACAGTGAAGACAATCCA 468

Qy      62  CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAATAATCCTGAGTAAGGTGGCCAC 121
      ||| | |  ||||| || ||  ||  | | | | | || |  ||
Db      467 ACAGCAGATAGAGGCTGGAAAGACCTTGTATTATTGATGTGATCTTAGGCAAAACAGCATG 408

Qy      122 TTTG 125
      ||||
Db      407 TTTG 404

```

RESULT 9

CF918988

LOCUS CF918988 579 bp mRNA linear EST 05-NOV-2003

DEFINITION Bflor531.000073 Amphioxus 26 hrs cDNA library (Name convention: BFL26 or MPMGp531) Branchiostoma floridae cDNA clone MPMGp531J1510;BFL26_10J15 5', mRNA sequence.

ACCESSION CF918988

VERSION CF918988.1 GI:38190190

KEYWORDS EST.

SOURCE Branchiostoma floridae (Florida lancelet)

ORGANISM Branchiostoma floridae
Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae; Branchiostoma.

REFERENCE 1 (bases 1 to 579)

AUTHORS Panopoulou,G., Hennig,S., Groth,D., Krause,A., Poustka,A.J., Herwig,R., Vingron,M. and Lehrach,H.

TITLE New evidence for genome-wide duplications at the origin of vertebrates using an amphioxus gene set and completed animal genomes

JOURNAL Genome Res. 13 (6A), 1056-1066 (2003)

PUBMED 12799346

COMMENT Contact: Panopoulou G
laboratory 145, dept.Lehrach

Max-Planck-Institut fuer Molekulare Genetik
Ihnestr.63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1235
Fax: +49 30 8413 1128

Email: panopoul@molgen.mpg.de

The library was characterised by oligonucleotide fingerprinting (ONFP) to reduce sequencing redundancy. According to the ONFP procedure clones giving the same hybridisation pattern with a battery of 200 8mer oligonucleotides are grouped into clusters. One clone per cluster is selected for sequencing. The size of each cluster is an indicator of the frequency of a transcript in the analysed library. The cluster size as well as the coordinates of all clones assigned to the same fingerprint cluster as the clone from which the above EST is generated is available at the amphioxus project site at <http://www.molgen.mpg.de/amphioxus>.

Clones and filters are distributed via the Resource Center/Primary Database of the German Genome Project (<http://www.rzpd.de>).

PCR Primers

FORWARD: 5' CCCCAGGCTTTACACTTTATGCTTCCGGCTCG 3' (M13RSP)

BACKWARD: 5' GCTATTACGCCAGCTGGCGAAAGGGGATGTG 3' (M13FSP)

Insert Length: 1200 Std Error: 200.00

Seq primer: 5'-CCGGTCCGGAATTCCTCGGGT-3' pSport3/86

High quality sequence stop: 579.

FEATURES

source

Location/Qualifiers

1. .579

/organism="Branchiostoma floridae"

/mol_type="mRNA"

/strain="wild type"

/db_xref="taxon:7739"

/clone="MPMGp531J1510;BFL26_10J15"

/tissue_type="whole embryo"

/dev_stage="26 hrs (neurula stage)"

/lab_host="Escherichia coli, XL1 blue"

/clone_lib="Amphioxus 26 hrs cDNA library (Name convention: BFL26 or MPMGp531)"

/note="Vector: pSport1; Site_1: SalI, KpnI, EcoRI (5');"

Site_2: NotI, BamHI, HindIII (3'); OligodT primed and

directionally cloned in pSport1 vector using a NotI

(5'-pGACTAGTTCTAGATCGCGAGCGGCCGCC (T)15-3' and a SalI 5'-

TCGACCCACGCGTCCG-3'adapters (Gibco BRL)."

ORIGIN

Query Match 25.0%; Score 31.2; DB 7; Length 579;

Best Local Similarity 57.0%; Pred. No. 27;

Matches 57; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

```
Qy      3 AAAACAAAAACCTTTACGTAACGTTTTTGCTGGGAGAGAAGACTACGAAGCACATTTTC 62
      || | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      339 AATTGACATAAGCTGTAGACACTTATTTTCTCCAAGGCAGGTCTTTGAATGAAACGTT 398

Qy      63 CAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACTAA 102
      || || | | | | | | | | | | | | | | | |
Db      399 AAGCAAGAGAGGACAGAAAAGAAGCTGAGCTTTTAAACAA 438
```

RESULT 10

BI285373/c

LOCUS BI285373 627 bp mRNA linear EST 19-JUL-2001

DEFINITION UI-R-DB0-byz-c-11-0-UI.s1 UI-R-DB0 Rattus norvegicus cDNA clone

UI-R-DB0-byz-c-11-0-UI 3', mRNA sequence.

ACCESSION BI285373

```

VERSION      BI285373.1   GI:14938944
KEYWORDS     EST.
SOURCE       Rattus norvegicus (Norway rat)
ORGANISM     Rattus norvegicus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
              Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE    1 (bases 1 to 627)
AUTHORS      Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE        Normalization and subtraction: two approaches to facilitate gene
              discovery
JOURNAL       Genome Res. 6 (9), 791-806 (1996)
PUBMED       8889548
COMMENT      Contact: Soares, MB
              Coordinated Laboratory for Computational Genomics
              University of Iowa
              375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
              Tel: 319 335 8250
              Fax: 319 335 9565
              Email: bento-soares@uiowa.edu
              The sequence contained an oligo-dT track that was present in the
              oligonucleotide that was used to prime the synthesis of first
              strand cDNA and therefore this may represent a bonafide poly A
              tail. The sequence tag present in the cDNA between the NotI site
              and the oligo-dT track served to verify it as a clone from the
              non-normalized bladder library cDNA Library Preparation: M.B.
              Soares Lab Clone distribution: clones will be available through
              Research Genetics (www.resgen.com)
              Seq primer: M13 Forward
              POLYA=Yes.

FEATURES             Location/Qualifiers
     source            1..627
                       /organism="Rattus norvegicus"
                       /mol_type="mRNA"
                       /strain="Sprague-Dawley"
                       /db_xref="taxon:10116"
                       /clone="UI-R-DB0-byz-c-11-0-UI"
                       /dev_stage="ADULT"
                       /lab_host="DH10B (Life Technologies)"
                       /clone_lib="UI-R-DB0"
                       /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                       polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-DB0
                       library is a non-normalized library constructed from rat
                       bladder tissue. For a detailed description of the library
                       from which this clone was derived, please visit our web
                       site at ratest.eng.uiowa.edu. The subtraction has been
                       previously described in (Bonaldo, Lennon and Soares,
                       Genome Research 6:791-806, 1996)
                       TAG_TISSUE=bladder
                       TAG_LIB=UI-R-DB0
                       TAG_SEQ=AGC"

```

Qy 62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACCTAATCCTGAGTAAGGTGGCCAC 121
 ||| | | |||| | | | | | | | | | | | |
 Db 465 ACAGCAGATAGAGGCTGGAAAGACCTTGTATTATTTGATGTGATCTTAGGCAAAACAGCATG 406
 Qy 122 TTTG 125
 ||||
 Db 405 TTTG 402

RESULT 11
 BI279004/c

LOCUS BI279004 630 bp mRNA linear EST 19-JUL-2001
 DEFINITION UI-R-DB0-byt-h-12-0-UI.s1 UI-R-DB0 Rattus norvegicus cDNA clone
 UI-R-DB0-byt-h-12-0-UI 3', mRNA sequence.

ACCESSION BI279004

VERSION BI279004.1 GI:14926402

KEYWORDS EST.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 630)

AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

PUBMED 8889548

COMMENT

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

The sequence contained an oligo-dT track that was present in the
 oligonucleotide that was used to prime the synthesis of first
 strand cDNA and therefore this may represent a bonafide poly A
 tail. The sequence tag present in the cDNA between the NotI site
 and the oligo-dT track served to verify it as a clone from the
 non-normalized bladder library cDNA Library Preparation: M.B.
 Soares Lab Clone distribution: clones will be available through
 Research Genetics (www.resgen.com)

Seq primer: M13 Forward

POLYA=Yes.

FEATURES

source

Location/Qualifiers

1. .630

/organism="Rattus norvegicus"

/mol_type="mRNA"

/strain="Sprague-Dawley"

/db_xref="taxon:10116"

/clone="UI-R-DB0-byt-h-12-0-UI"

/dev_stage="ADULT"

/lab_host="DH10B (Life Technologies)"

/clone_lib="UI-R-DB0"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-DB0
 library is a non-normalized library constructed from rat
 bladder tissue. For a detailed description of the library
 from which this clone was derived, please visit our web
 site at ratest.eng.uiowa.edu. The subtraction has been

previously described in (Bonaldo, Lennon and Soares,
Genome Research 6:791-806, 1996)
TAG_TISSUE=bladder
TAG_LIB=UI-R-DB0
TAG_SEQ=AGC"

ORIGIN

Query Match 25.0%; Score 31.2; DB 2; Length 630;
Best Local Similarity 53.2%; Pred. No. 28;
Matches 66; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

Qy 2 AAAAACAAAAACCTTTACGTAAACGTTTTTGTGGGAGAGAAGACTACGAAGCACATTTT 61
||| | | | | | | | | | | | | | | | | | | |
Db 526 AAACAACAGTGACTTGATCTAAGTCGTGTGGTGAAGTGAAGACAGTGAAGACAATCCA 467

Qy 62 CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACCTAATCCTGAGTAAGGTGGCCAC 121
||| | | | | | | | | | | | | | | | | | | |
Db 466 ACAGCAGATAGAGGCTGGAAAGACCTTGTTATTTGATGTGATCTTAGGCAAAACAGCATG 407

Qy 122 TTTG 125
||| |
Db 406 TTTG 403

RESULT 12 BI285082/c

LOCUS BI285082 655 bp mRNA linear EST 19-JUL-2001
DEFINITION UI-R-DB0-byw-a-02-0-UI.s1 UI-R-DB0 Rattus norvegicus cDNA clone
UI-R-DB0-byw-a-02-0-UI 3', mRNA sequence.
ACCESSION BI285082
VERSION BI285082.1 GI:14938372
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 655)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
PUBMED 8889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to verify it as a clone from the
non-normalized bladder library cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com) The following repetitive
elements were found in this cDNA sequence: 1-21,
>AT_rich#Low_complexity
Seq primer: M13 Forward


```

FEATURES
  source
    Location/Qualifiers
      1. .655
        /organism="Rattus norvegicus"
        /mol_type="mRNA"
        /strain="Sprague-Dawley"
        /db_xref="taxon:10116"
        /clone="UI-R-DB0-byw-a-02-0-UI"
        /dev_stage="ADULT"
        /lab_host="DH10B (Life Technologies)"
        /clone_lib="UI-R-DB0"
        /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-DB0
library is a non-normalized library constructed from rat
bladder tissue. For a detailed description of the library
from which this clone was derived, please visit our web
site at ratest.eng.uiowa.edu. The subtraction has been
previously described in (Bonaldo, Lennon and Soares,
Genome Research 6:791-806, 1996)
TAG_TISSUE=bladder
TAG_LIB=UI-R-DB0
TAG_SEQ=AGC"

```

Query Match 25.0%; Score 31.2; DB 2; Length 655;
Best Local Similarity 53.2%; Pred. No. 28;
Matches 66; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

Qy	2	AAAAACAAAAACCTTTACGTAACGTTTTTGTCTGGGAGAGAAGACTACGAAGCACATTTT	61
Db	537	AAACAACAGTGACTTGTATCTAAGTCGTGTGGTGGGAAGTGAAGACAGTGAAGACAATCCA	478
Qy	62	CCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAATAATCCTGAGTAAGGTGGCCAC	121
Db	477	ACAGCAGATAGAGGCTGGAAAGACCTTGTTATTGTATGTGATCTTAGGCCAAAACAGCATG	418
Qy	122	TTTG	125
Db	417	TTTG	414

```

CW685817
LOCUS         CW685817             669 bp      DNA      linear      GSS 01-NOV-2004
DEFINITION    OG_BBa0044A23.f OG_BBa Oryza glaberrima genomic clone OG_BBa0044A23
              5', genomic survey sequence.
ACCESSION     CW685817
VERSION       CW685817.1  GI:55155379
KEYWORDS      GSS.
SOURCE        Oryza glaberrima (African rice)
              ORGANISM  Oryza glaberrima
                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                  Ehrhartoideae; Oryzeae; Oryza.
REFERENCE     1 (bases 1 to 669)
AUTHORS       Kim,H., Yu,Y., Wissotski,M., Byrne,M., Stum,D., Smart,D., Rao,K.,
              Luo,M., Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C.
              and Wing,R.
TITLE         OMAP
JOURNAL       Unpublished (2004)
COMMENT       Contact: Rod A. Wing

```

```

FEATURES                                Location/Qualifiers
     source                               1. .669
                                         /organism="Oryza glaberrima"
                                         /mol_type="genomic DNA"
                                         /db_xref="taxon:4538"
                                         /clone="OG_BBa0044A23"
                                         /tissue_type="young leaves"
                                         /lab_host="DH10B T1 phage resistant"
                                         /clone_lib="OG_BBa"
                                         /note="Vector: pAGIBAC1; Site 1: HindIII; Site 2: HindIII"

```

Query Match 24.8%; Score 31; DB 10; Length 669;
Best Local Similarity 59.8%; Pred. No. 33;
Matches 52; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Fax: 919 613 8177
Email: chauser@duke.edu.

FEATURES
source Location/Qualifiers
1. .422
/organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
/strain="CC-1690 wild type mt+ 2lgr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap II"
/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2: XhoI; This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP (acetate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in ambient levels of CO₂ and HS medium bubbled with 5% CO₂. PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."

ORIGIN

Query Match 24.6%; Score 30.8; DB 3; Length 422;
Best Local Similarity 70.7%; Pred. No. 34;
Matches 41; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 61 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACCTAATCCTGAGTAAGGTGGC 118
|| || || |||| |||| || ||||| || || || |||||
Db 264 TCATGGCAGCATGGGATGCACCGCGTGTGCGCTCTGCACACGTCGTGGGTGAGGTGGC 207

RESULT 15
BI999848/c
LOCUS BI999848 452 bp mRNA linear EST 25-OCT-2001
DEFINITION 1031079E03.x2 C. reinhardtii CC-1690, Stress II (normalized), Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
ACCESSION BI999848
VERSION BI999848.1 GI:16434622
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii
ORGANISM Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae;
Chlamydomonadales; Chlamydomonadaceae; Chlamydomonas.
REFERENCE 1 (bases 1 to 452)
AUTHORS Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C., Lefebvre, P., McDermott, J.P., Shrager, J., Silflow, C. and Stern, D.
TITLE Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants. Project: 1031
JOURNAL Unpublished (2001)
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Durham, NC 27708-1000
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Fax: 919 613 8177
Email: chauser@duke.edu.
FEATURES Location/Qualifiers

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source      1. .452
            /organism="Chlamydomonas reinhardtii"
            /mol_type="mRNA"
            /strain="CC-1690 wild type mt+ 2lgr"
            /db_xref="taxon:3055"
            /clone_lib="C. reinhardtii CC-1690, Stress II
            (normalized), Lambda Zap II"
            /note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
            XhoI; Stress condition II library, constructed by John
            Davies and Jeffrey McDermott, combines cDNAs from CC-1690
            cells grown to mid-log phase in TAP (NH4+ - containing)
            and shifted to TAP - NO3- (24hrs); H2 production
            conditions (0, 12hr, 24hr) see Melis et al., (2000) Plant
            Phys. 122: 127-135; TAP + H2O2 (1, 12, 24 hr); TAP +
            sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr).
            PolyA mRNA was purified from each sample, pooled and cDNA
            synthesized. The cDNA was directionally cloned into lambda
            Zap II (Stratagene) in the EcoRI (5') and XhoRI (3')
            sites. pBluescript II SK- plasmids were excised from the
            lambda ZAP clones by superinfection with ExAssist
            (Stratagene) phage. The library was normalized using
            method 4 described in Bonaldo et al., (1996) Genome
            Research 6: 791-806."

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ORIGIN

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Query Match          24.6%;  Score 30.8;  DB 3;  Length 452;
Best Local Similarity 70.7%;  Pred. No. 35;
Matches 41;  Conservative 0;  Mismatches 17;  Indels 0;  Gaps 0;

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Qy      61 TCCAGGAAGTGTGGGCTGCAACGATTGTGCGCTCTTAACCTAGTAAGGTGGC 118
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Db      265 TCATGGCAGCATGGGATGCACCGCGTGTGCGCTCTGCACACGTCGTGGGTGAGGTGGC 208

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Search completed: April 25, 2006, 10:52:01
Job time : 1991 secs

SCORE 1.3 BuildDate: 12/06/2005
